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Date completed: 05-29-03
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20 ; Search time 29.333 Seconds
(without alignments)
99.938 Million cell updates/sec

Title: US-09-147-362A-2

Sequence: 127
1 LSLWGRKRLVCTSVQNMET 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 101002:*

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22:	/SID2/gcgdata/geneseq/geneeqp-emb1/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	127	100.0	22	19	AAW80460	Peptide derived fr
2	122	96.1	22	19	AAW80465	Peptide derived fr
3	121	95.3	22	19	AAW80466	Peptide derived fr
4	119	93.7	22	19	AAW80459	Peptide derived fr
5	119	93.7	22	19	AAW80471	Peptide derived fr
6	118	92.9	22	19	AAW80461	Peptide derived fr
7	118	92.9	32	19	AAW80470	Peptide derived fr
8	116	91.3	113	20	AAV05565	HIV-1 group O isol
9	116	91.3	200	21	AAV77373	HIV-1 group O env
10	116	91.3	215	20	AAV09499	HIV-1 group O env

11	116	91.3	215	20	AAV06983	Recombinant pG0-8P
12	116	91.3	215	21	AAV77374	HIV-1 group O env
13	116	91.3	245	20	AAV09493	HIV-1 group O env
14	116	91.3	245	20	AAV06977	Recombinant pG0-9P
15	116	91.3	245	21	AAV77369	HIV-1 group O pG0-9P
16	116	91.3	281	20	AAV09507	HIV-1 group O env
17	116	91.3	373	20	AAV09495	HIV-1 group O env
18	116	91.3	373	20	AAV06979	Recombinant pG0-11
19	116	91.3	460	20	AAV09500	HIV-1 group O env
20	116	91.3	460	20	AAV06984	Recombinant pG0-8C
21	116	91.3	460	21	AAV77375	HIV-1 group O env
22	116	91.3	474	21	AAV77371	HIV-1 group O env
23	116	91.3	488	20	AAV09504	HIV-1 group O env
24	116	91.3	490	20	AAV09494	Recombinant pG0-9C
25	116	91.3	490	20	AAV06978	HIV-1 group O env
26	116	91.3	490	21	AAV77370	HIV-1 group O poly
27	116	91.3	526	20	AAV09505	HIV-1 group O env
28	116	91.3	618	20	AAV09496	Recombinant pG0-11
29	116	91.3	618	20	AAV06980	HIV-1 group O env
30	116	91.3	618	21	AAV77372	HIV-1 group O env
31	116	91.3	706	20	AAV09503	HIV-1 group M and
32	116	91.3	715	20	AAV05625	HIV-1 group M and
33	116	91.3	736	20	AAV09502	HIV-1 group O env
34	116	91.3	873	20	AAV09501	Amino acid sequenc
35	116	91.3	873	20	AAV05985	HIV-1 group O isol
36	116	91.3	873	21	AAV77376	HIV-1 group O beta
37	115	90.6	104	19	AAW07245	Peptide derived fr
38	114	89.8	32	19	AAW80469	Peptide derived fr
39	113	89.0	22	19	AAW80462	HIV-1 group O isol
40	113	89.0	113	20	AAV05559	HIV-1 group O isol
41	113	89.0	116	20	AAV05555	gp 41 antigen of H
42	113	89.0	356	17	AAW03940	HIV-1 group O isol
43	112	88.2	113	20	AAV05554	HIV-1 group O isol
44	112	88.2	113	20	AAV05546	HIV-1 group O isol
45	112	88.2	117	20	AAV05548	HIV-1 group O isol

ALIGNMENTS

RESULT 1
AAW80460 standard; peptide; 22 AA.

XX	AAW80460;
XX	28-JAN-1999 (first entry)
XX	Peptide derived from a conserved sequence of group O human HIV.
XX	Group O human immune deficiency virus; HIV; detection; infection.
XX	Synthetic.
XX	Immune deficiency virus.
XX	W09845323-A1.
XX	15-OCT-1998.
XX	06-APR-1998; 98WO-FR00691.
XX	24-FEB-1998; 98FR-0002212.
XX	09-APR-1997; 97FR-0004356.
XX	(SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
XX	Cherebaux DMB, Delagneau JFH, Gadelle SUV, Rieunier FY;
XX	WPI, 1998-583190/49.
XX	New synthetic peptide(s) - useful for, e.g. detecting infection by
XX	human immune deficiency virus of group O
XX	

PS Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 127; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
 DB 1 LLSLMGCRGLVCTSVQNMET 22

AAW80465
 LT 2

ID AAW80465 standard; peptide; 22 AA.

AC AAW80465;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

XX Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

XX 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Riennier FY;

WPI, 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O

XX Claim 6; Page 43; 55pp; French.

AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX

SQ Sequence 22 AA;

Query Match 96.1%; Score 122; DB 19; Length 22;
 Best Local Similarity 95.5%; Pred. No. 8.3e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
 DB 1 LLSLMGCRGLVCTSVQNMET 22

RESULT 3

ID AAW80466 standard; peptide; 22 AA.

AC AAW80466;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

XX Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

XX 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Riennier FY;

WPI, 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O

XX Claim 6; Page 43; 55pp; French.

AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX

SQ Sequence 22 AA;

Query Match 95.3%; Score 121; DB 19; Length 22;
 Best Local Similarity 95.5%; Pred. No. 1.1e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
 DB 1 LLSLMGCRGLVCTSVQNMET 22

RESULT 4

ID AAW80459 standard; peptide; 22 AA.

AC AAW80459;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

XX Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

XX 24-FEB-1998; 98FR-0002212.
 PR 09-APR-1997; 97FR-0004356.
 XX
 PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 PI Chenebaux DMB, Delagneau JFH, Gadelie SXJ, Rieunier FY;
 XX WPI; 1998-583190/49.
 DR
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 PS Claim 6; Page 42; 55pp; French.
 CC AAM80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 22 AA;
 Query Match 93.7%; Score 119; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2.1e-09;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 LLSLMGCRGLVCTSVQNMET 22
 1 LLSLMGCRGKAVCTSVQNMET 22
 DB
 RESULT 5
 AAM80471
 ID AAM80471 standard; peptide; 32 AA.
 XX
 AC AAM80471;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Peptide derived from a conserved sequence of group O human HIV.
 XX
 KM Group O human immune deficiency virus; HIV; detection; infection.
 XX
 OS Synthetic.
 OS Immune deficiency virus.
 XX
 WO9845323-A1.
 PD 15-OCT-1998.
 XX
 PF 06-APR-1998; 98WO-FR00691.
 XX
 PR 24-FEB-1998; 98FR-0002212.
 PR 09-APR-1997; 97FR-0004356.
 XX
 PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 PI Chenebaux DMB, Delagneau JFH, Gadelie SXJ, Rieunier FY;
 XX WPI; 1998-583190/49.
 DR
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 PS Claim 6; Page 44; 55pp; French.
 CC AAM80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O

CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 32 AA;
 Query Match 93.7%; Score 119; DB 19; Length 32;
 Best Local Similarity 90.9%; Pred. No. 3e-09;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 LLSLMGCRGLVCTSVQNMET 22
 1 LLSLMGCRGLVCTSVQNMET 32
 DB
 RESULT 6
 AAM80461
 ID AAM80461 standard; peptide; 22 AA.
 XX
 AC AAM80461;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Peptide derived from a conserved sequence of group O human HIV.
 XX
 KM Group O human immune deficiency virus; HIV; detection; infection.
 XX
 OS Synthetic.
 OS Immune deficiency virus.
 XX
 WO9845323-A1.
 PD 15-OCT-1998.
 XX
 PF 06-APR-1998; 98WO-FR00691.
 XX
 PR 24-FEB-1998; 98FR-0002212.
 PR 09-APR-1997; 97FR-0004356.
 XX
 PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 PI Chenebaux DMB, Delagneau JFH, Gadelie SXJ, Rieunier FY;
 XX WPI; 1998-583190/49.
 DR
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 PS Claim 6; Page 42; 55pp; French.
 CC AAM80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 22 AA;
 Query Match 92.9%; Score 118; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2.9e-09;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 LLSLMGCRGLVCTSVQNMET 22
 1 LLSLMGCRGRLVCTSVQNMET 22
 DB
 RESULT 7
 AAM80470
 ID AAM80470 standard; peptide; 32 AA.
 XX
 AC AAM80470;
 XX
 DT 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.
 DE Group O human immune deficiency virus; HIV; detection; infection.
 KW Synthetic.
 XX Immune deficiency virus.
 OS
 XX WO9845323-A1.
 PN
 XX
 PD 15-OCT-1998.
 XX
 PF 06-APR-1998; 98WO-FR00691.
 XX
 PR 24-FEB-1998; 98PR-0002212.
 PR 09-APR-1997; 97PR-0004356.
 XX
 PA (SNF1) PASTEUR SANOFI DIAGNOSTICS SA.
 XX
 DR Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;
 DR WPI; 1998-583190/49.
 XX
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX
 PS Claim 6; Page 44; 55pp; French.
 XX
 CC AAM90459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 32 AA;
 QY
 Query Match 92.9%; Score 118; DB 19; Length 32;
 Best Local Similarity 86.4%; Pred. No. 4.1e-09;
 Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 DB 11 L1LTMGCRRLVCTYSVNMNET 22
 11 L1LTMGCRRLVCTYSVNMNET 32
 RESULT 8
 AAY05565
 AAY05565 standard; Protein; 113 AA.
 AC AAY05565;
 DT 19-JUL-1999 (first entry)
 XX
 DE HIV-1 group O isolate MP539-PBMC gp41 antigen.
 XX
 KW HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
 KW vaccine; diagnosis; AIDS.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 65 /note= "encoded by AMW"
 FT Misc-difference 74 /note= "encoded by ATR"
 FT Misc-difference 84 /note= "encoded by GAK"
 FT Misc-difference 86 /note= "encoded by AGY"
 FT
 PN WO9904011-A2.
 XX

PD 28-JAN-1999.
 XX
 PF 20-JUL-1998; 98WO-EP04522.
 XX
 FR 18-JUL-1997; 97EP-0870110.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
 PI WPI; 1999-132255/11.
 DR N-PSDB; AAY05565.
 XX
 PT New isolated HIV-1 group O strains - used to produce
 PT polynucleotides, antigens and antibodies for use in diagnosis and in
 PT vaccines for prevention of HIV-1 infection
 XX
 PS Claim 3; Fig 6; 162pp; English.
 XX
 CC The present sequence is an antigen of the gp41 protein of HIV-1
 CC group O (Outlier) strain MP539-PBMC, a Cameroon isolate. The
 CC invention relates to new HIV-1 group O antigens (see AAY05546-625),
 CC and the use of these antigens, or nucleic acids encoding them (see
 CC AAY25154-80), in the diagnosis and prophylaxis of AIDS. They can be
 CC used as reagents for detecting HIV-1 group O infection and for
 CC differentiating different types of HIV-1 group O infection.
 CC Vaccines that provide protective immunity against HIV-1 infection,
 CC particular against HIV-1 group O infection, comprise at least one
 CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a
 CC virus-like particle comprising such an antigen, or an attenuated
 CC form of an HIV-1 type O strain. The invention also relates to new
 CC HIV-1 group O strains, mostly from patients from Cameroon and its
 CC neighbouring countries.
 XX
 SQ Sequence 113 AA;
 QY
 Query Match 91.3%; Score 116; DB 20; Length 113;
 Best Local Similarity 81.8%; Pred. No. 2.5e-08;
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 DB 39 L1LTMGCRRLVCTYSVNMNET 60
 1 L1LTMGCRRLVCTYSVNMNET 22
 39 L1LTMGCRRLVCTYSVNMNET 60
 RESULT 9
 AAY77373
 AAY77373 standard; Protein; 200 AA.
 AC AAY77373;
 DT 22-MAY-2000 (first entry)
 XX
 DE HIV-1 group O env gp120/gp41 pCO-5 recombinant protein, SEQ ID NO:56.
 XX
 KW HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;
 KW immunosay; positive control; affinity purification; therapeutic;
 KW Escherichia coli; antigen; synthetic gene construction; muten;
 KW deletion mutation.
 XX
 OS Human immunodeficiency virus type 1 group O isolate HAM112.
 OS Synthetic.
 XX
 PN WO200004383-A2.
 XX
 PD 27-JAN-2000.
 XX
 PF 09-JUL-1999; 99WO-US15469.
 PF
 PR 14-JUL-1998; 98US-0115171.
 PR
 XX (ABBO) ABBOTT LAB.
 PA
 XX

PI Scheffel JW, Hackett JR, Tyner JD, Hickman RK;
 XX WPI: 2000-171290/15.
 DR N-PSDB; AAZ90284.
 XX
 PT Novel monoclonal antibodies useful as positive control reagent for
 PT detecting human immunodeficiency virus infections and diagnosing,
 PT evaluating or prognosing viral disease -
 XX
 XX Example 3; Fig 9, 148pp; English.
 PS
 CC The invention relates to anti-HIV-1 group O monoclonal antibodies, which
 CC may be used as positive control reagents in immunoassays to detect and
 CC differentiate HIV-1 infections. The invention also encompasses a
 CC monoclonal antibody which binds specifically to an HIV-1 group O
 CC antigen, which has no more than 15% cross reactivity to a corresponding
 CC antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a
 CC method of using a monoclonal antibody as a positive control reagent in
 CC an immunoassay for the detection of anti HIV-1 group O antibodies. The
 CC monoclonal antibodies are useful as positive control reagents in
 CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such
 CC immunoassays involve coupling a monoclonal antibody with HIV group-1
 CC antigen and detecting the antigen-antibody complex. The monoclonal
 CC antibodies of the invention would be used to ensure that the reagents
 CC provided to detect HIV-1 group O antibody were performing properly. The
 CC monoclonal antibodies may also can be immobilised on a matrix and used
 CC for affinity purification of specific HIV-1 group O-derived proteins
 CC from cell cultures or biological tissues. The monoclonal antibodies can
 CC also be used for generating chimeric antibodies for therapeutic use.
 CC Different synthetic, recombinant or purified antibodies which identify
 CC different epitopes of HIV antigens can be used in combination in assay to
 CC diagnose, evaluate, or prognosticate HIV disease condition. The
 CC monoclonal antibodies are also useful for differentiating HIV-1 Group O
 CC antigens from HIV-group M and HIV-2 antigens. Sequences AA77369-77375
 CC represent recombinant HIV-1 group O env antigens encoded by the synthetic
 CC genes AAZ90280-290286. The recombinant HIV-1 env proteins contain
 CC various deletions relative to the native HAM12 isolate env protein
 CC (AA77376). The recombinant HIV-1 group O antigens were purified and used
 CC to screen hybridoma cultures.
 CC
 SQ Sequence 200 AA:
 Query Match 91.3%; Score 116; DB 21; Length 200;
 Best Local Similarity 81.8%; Pred. No. 4.4e-08;
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCGRLVCTSVQNNET 22
 112 LLLMWGCKGRLICTSVKNNET 133

RESULT 10
 ID AA09499 standard; Protein; 215 AA.
 AC AAY09499;
 XX
 DT 15-JUL-1999 (first entry)
 XX
 DE HIV-1 Group O env polypeptide pGO-8PL.
 XX
 KM HIV; human immunodeficiency virus; antigen; detection; antibody;
 KM differentiation; Group O; env; immunogen; immunoassay.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9909179-A2.
 XX
 PD 25-FEB-1999.
 XX
 PF 17-AUG-1998; 98WO-US17014.
 XX
 PR 15-AUG-1997; 97US-0911824.

XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;
 XX WPI: 1999-190167/16.
 DR N-PSDB; AAZ56078.
 XX
 PT New isolated HIV-1 Group O env polypeptides - used for the
 PT detection of anti-HIV antibodies and for the production of
 PT antibodies for use in detection, purification and therapy
 XX
 XX Claim 17; Fig 5; 138pp; English.
 PS
 CC The present invention describes (A) an isolated HIV-1 Group O env
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in
 CC (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) an
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a
 CC second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as
 CC in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a
 CC host cell transformed by an expression vector as in (8); and (10) an
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an
 CC antigen construct as in (3)-(6). The antigen constructs can be used for
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be
 CC used as immunogens to produce antibodies. The antibodies can be used to
 CC purify HIV polypeptides, for therapy and for detection of HIV
 CC polypeptides.
 CC
 SQ Sequence 215 AA:
 Query Match 91.3%; Score 116; DB 20; Length 215;
 Best Local Similarity 81.8%; Pred. No. 4.7e-08;
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCGRLVCTSVQNNET 22
 Db 127 LLLMWGCKGRLICTSVKNNET 148

RESULT 11
 ID AA06983 standard; Protein; 215 AA.
 AC AAY06983;
 XX
 DT 06-JUL-1999 (first entry)
 XX
 DE Recombinant pGO-8PL protein.
 XX
 KM HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;
 KM antibody; assay.
 XX
 OS Synthetic.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 FH Key Location/Qualifiers
 FH Protein 2..46
 FT /note= "gp120 sequence"
 FT 47..245
 FT Peptide /note= "gp41 sequence"
 XX
 PN WO9909410-A2.
 XX
 PD 25-FEB-1999.
 XX
 PF 07-AUG-1998; 98WO-US16506.

XX 15-AUG-1997; 97US-0912129.
 PR (ABBO) ABBOTT LAB.
 XX
 PA Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;
 PI Necklows EC, Vallari AS, Varilek V,
 XX WPI: 1999-190224/16.
 DR N-PSDB; AAX37193.
 XX
 PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
 PT can be used in field assay, requiring no electricity and less
 PT specialised equipment
 XX
 PS Claim 1; Fig 5; 104pp; English.
 XX
 CC The invention relates to a rapid assay for simultaneous detection and
 CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
 CC method comprises (a) contacting the sample with a strip containing at
 CC least one immobilised capture reagent per analyte and on which the
 CC sample moves from the proximal to the distal end by capillary action,
 CC and (b) determining the presence of analyte(s) by detecting a visible
 CC colour change at the capture reagent site on the strip wherein the
 CC capture reagent for HIV-1 group O comprises a polypeptide shown in
 CC AA06977-80 and AA06983-84; and that for HIV-1 group M comprises a
 CC polypeptide shown in AA06982; and that for HIV-2 comprises the
 CC for antibodies to HIV-1 types O and M, and HIV-2. The invention will be
 CC particularly useful in places and situation where equipment and/or
 CC electricity is not available. The invention provides a screening method
 CC which is faster and requires less equipment than prior art methods. The
 CC present sequence represents a amino acid sequence of the recombinant
 CC PGO-8PL protein which acts as a capture reagent for HIV-1 group O.
 XX
 SQ Sequence 215 AA;
 XX
 QY Query Match 91.3%; Score 116; DB 20; Length 215;
 DB Best Local Similarity 81.8%; Pred. No. 4.7e-08;
 DB Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 DB 1 LSLMCGRGLVCYTSVKNMET 22
 DB 127 LNLNMGCKRGLCYTSVKNMET 148
 XX
 XX JUL 12
 XX 7374
 XX AA077374 standard; Protein; 215 AA.
 XX
 XX AA077374;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE HIV-1 group O env gp120/gp41 PGO-8PL recombinant protein, SEQ ID NO:58.
 XX
 KW HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;
 KW immunodassay; positive control; affinity purification; therapeutic;
 KW Escherichia coli; antigen; synthetic gene construction; mucin;
 KW deletion mutation.
 XX
 OS Human immunodeficiency virus type 1 group O isolate HAM112.
 OS Synthetic.
 XX
 EN WO200004383-A2.
 XX
 PD 27-JAN-2000.
 XX
 PE 09-JUL-1999; 99WO-US15469.
 XX
 PR 14-JUL-1998; 98US-0115171.
 XX

PA (ABBO) ABBOTT LAB.
 XX
 XX Scheffel JW, Hackett JR, Tyner JD, Hickman RK;
 XX WPI: 2000-171290/15.
 DR N-PSDB; AA290285.
 XX
 PT Novel monoclonal antibodies useful as positive control reagent for
 PT detecting human immunodeficiency virus infections and diagnosing,
 PT evaluating or prognosing viral disease -
 XX
 PS Example 3; Fig 5; 148pp; English.
 XX
 CC The invention relates to anti-HIV-1 group O monoclonal antibodies, which
 CC may be used as positive control reagents in immunoassays to detect and
 CC differentiate HIV-1 infections. The invention also encompasses a
 CC monoclonal antibody which binds specifically to an HIV-1 group O
 CC antigen, which has no more than 15% cross reactivity to a corresponding
 CC antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a
 CC method of using a monoclonal antibody as a positive control reagent in
 CC an immunoassay for the detection of anti HIV-1 group O antibodies. The
 CC monoclonal antibodies are useful as positive control reagents in
 CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such
 CC immunoassays involve coupling a monoclonal antibody with HIV group-1
 CC antigen and detecting the antigen-antibody complex. The monoclonal
 CC antibodies of the invention would be used to ensure that the reagents
 CC provided to detect HIV-1 group O antibody were performing properly. The
 CC monoclonal antibodies may also can be immobilised on a matrix and used
 CC from cell cultures or biological tissues. The monoclonal antibodies can
 CC also be used for generating chimeric antibodies for therapeutic use.
 CC Different epitopes of HIV antigens can be used in combination in assay to
 CC diagnose, evaluate, or prognosticate HIV disease condition. The
 CC monoclonal antibodies are also useful for differentiating HIV-1 group O
 CC antigens from HIV-group M and HIV-2 antigens. Sequences AA077369-77375
 CC represent recombinant HIV-1 group O env antigens encoded by the synthetic
 CC genes AA090280-290286. The recombinant HIV-1 env proteins contain
 CC various deletions relative to the native HAM112 isolate env protein
 CC (AA077376). The recombinant HIV-1 group O antigens were purified and used
 CC to screen hybridoma cultures.
 XX
 SQ Sequence 215 AA;
 XX
 QY Query Match 91.3%; Score 116; DB 21; Length 215;
 DB Best Local Similarity 81.8%; Pred. No. 4.7e-08;
 DB Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 DB 1 LSLMCGRGLVCYTSVKNMET 22
 DB 127 LNLNMGCKRGLCYTSVKNMET 148
 XX
 XX RESULT 13
 XX AA09493
 XX ID AA09493 standard; Protein; 245 AA.
 XX
 XX AA09493;
 XX
 DT 15-JUL-1999 (first entry)
 XX
 DE HIV-1 Group O env polypeptide PGO-9PL.
 XX
 KW HIV; human immunodeficiency virus; antigen; detection; antibody;
 KW differentiation; Group O; env; immunogen; immunoassay.
 XX
 OS Human immunodeficiency virus type 1.
 OS
 XX
 PD WO9909179-A2.
 XX
 PE 25-FEB-1999.
 XX
 PR 17-AUG-1998; 98WO-US17014.
 XX

XX 15-AUG-1997; 97US-0911824.
 XX (ABBO) ABBOTT LAB.
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;
 XX WPI; 1999-190167/16.
 XX N-PSDB; AAX56074.
 XX New isolated HIV-1 Group O env polypeptides - used for the
 XX detection of anti-HIV antibodies and for the production of
 XX antibodies for use in detection, purification and therapy
 XX Claim 16; Fig 7, 138pp; English.
 XX The present invention describes (A) an isolated HIV-1 Group O env
 XX polypeptide. Also described are: (1) an isolated HIV-1 Group O env
 XX polypeptide comprising an immunoreactive portion of a polypeptide as in
 XX (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);
 XX (3) an antigen construct comprising a first HIV-1 Group O env polypeptide
 XX fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
 XX comprising a fusion of at least one HIV-1 Group O env polypeptide with at
 XX least one HIV-1 Group M env polypeptide; (5) an antigen construct
 XX comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env
 XX polypeptide, and at least one additional HIV-1 polypeptide; (6) an
 XX antigen construct comprising a first HIV-2 env polypeptide fused to a
 XX second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as
 XX in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a
 XX host cell transformed by an expression vector as in (8); and (10) an
 XX immunoassay kit for the detection of antibodies to HIV-1 comprising an
 XX antigen construct as in (3)-(6). The antigen constructs can be used for
 XX the detection of anti-HIV-1 antibodies in test samples. They can also be
 XX used as immunogens to produce antibodies. The antibodies can be used to
 XX purify HIV polypeptides, for therapy and for detection of HIV
 XX polypeptides.
 XX Sequence 245 AA;
 XX
 XX Query Match 91.3%; Score 116; DB 20; Length 245;
 XX Best Local Similarity 81.8%; Pred. No. 5.3e-08;
 XX Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LLSLMGCGRLVCYTSVQNNET 22
 DB 127 LLLMGGCKGRLLCYTSVKNNET 148
 XX
 XX LT 14
 XX 6977
 XX ID AAY06977 standard; Protein; 245 AA.
 XX AC AAY06977;
 XX DT 06-JUL-1999 (first entry)
 XX DE Recombinant pGO-9PL protein.
 XX HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;
 XX antibody; assay.
 XX Synthetic.
 XX OS Human immunodeficiency virus type 1.
 XX Key Location/Qualifiers
 XX Protein 2..46
 XX /note= "gp120 sequence"
 XX Peptide 47..245
 XX /note= "gp41 sequence"
 XX WO9909410-A2.
 XX 25-FEB-1999.
 XX PD

XX 07-AUG-1998; 98WO-US16506.
 XX 15-AUG-1997; 97US-0912129.
 XX (ABBO) ABBOTT LAB.
 XX Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;
 XX Necklawa EC, Vallari AS, Varilek V;
 XX WPI; 1999-190224/16.
 XX N-PSDB; AAX37189.
 XX New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
 XX can be used in field assay, requiring no electricity and less
 XX specialised equipment
 XX Claim 1; Fig 7, 104pp; English.
 XX The invention relates to a rapid assay for simultaneous detection and
 XX differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
 XX method comprises (a) contacting the sample with a strip containing at
 XX least one immobilised capture reagent per analyte and on which the
 XX sample moves from the proximal to the distal end by capillary action,
 XX under conditions sufficient to form capture reagent/analyte complexes,
 XX and (b) determining the presence of analyte(s) by detecting a visible
 XX colour change at the capture site on the strip wherein the
 XX capture reagent for HIV-1 group O comprises a polypeptide shown in
 XX AAY06977-80 and AAY06983-84; and that for HIV-1 group M comprises a
 XX polypeptide shown in AAY06981. The invention is used to screen patients
 XX for antibodies to HIV-1 types O and M, and HIV-2. The invention will be
 XX particularly useful in places and situation where equipment and/or
 XX electricity is not available. The invention provides a screening method
 XX which is faster and requires less equipment than prior art methods. The
 XX present sequence represents a amino acid sequence of the recombinant
 XX pGO-9PL recombinant protein which acts as a capture reagent for HIV-1
 XX group O.
 XX Sequence 245 AA;
 XX
 XX Query Match 91.3%; Score 116; DB 20; Length 245;
 XX Best Local Similarity 81.8%; Pred. No. 5.3e-08;
 XX Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LLSLMGCGRLVCYTSVQNNET 22
 DB 127 LLLMGGCKGRLLCYTSVKNNET 148
 XX
 XX RESULT 15
 XX AAY77369
 XX ID AAY77369 standard; Protein; 245 AA.
 XX AC AAY77369;
 XX DT 22-MAY-2000 (first entry)
 XX DE HIV-1 group O pGO-9PL encoded truncated env gp41 protein, SEQ ID NO:48.
 XX HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;
 XX immunoassay; positive control; affinity purification; therapeutic;
 XX Escherichia coli; antigen; synthetic gene construction; mutcin;
 XX deletion mutation.
 XX Synthetic.
 XX OS Human immunodeficiency virus type 1 group O isolate HAM112.
 XX WO200004381-A2.
 XX 27-JAN-2000.
 XX 09-JUL-1999; 99WO-US15469.
 XX PD

XX 14-JUL-1998; 98US-0115171.
 PR (ABBO) ABBOTT LAB.
 PA
 XX Scheffel JW, Hackett JR, Tyner JD, Hickman RK;
 PI
 XX WPI; 2000-171290/15.
 DR N-PSDB; AA290280.
 PT Novel monoclonal antibodies useful as positive control reagent for
 PT detecting human immunodeficiency virus infections and diagnosing,
 XX evaluating or prognosing viral disease.
 PS Example 3; Page 120-121; 148pp; English.
 XX
 CC The invention relates to anti-HIV-1 group O monoclonal antibodies, which
 CC may be used as positive control reagents in immunoassays to detect and
 CC differentiate HIV-1 infections. The invention also encompasses a
 CC monoclonal antibody which binds specifically to an HIV-1 group O
 CC antigen, which has no more than 15% cross reactivity to a corresponding
 CC antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a
 CC method of using a monoclonal antibody as a positive control reagent in
 CC an immunoassay for the detection of anti HIV-1 group O antibodies. The
 CC monoclonal antibodies are useful as positive control reagents in
 CC immunoassays capable of detecting anti-HIV-1 Group O antibodies. Such
 CC immunoassays involve coupling a monoclonal antibody with HIV group-O
 CC antigen and detecting the antigen-antibody complex. The monoclonal
 CC antibodies of the invention would be used to ensure that the reagents
 CC provided to detect HIV-1 group O antibody were performing properly. The
 CC monoclonal antibodies may also can be immobilised on a matrix and used
 CC for affinity purification of specific HIV-1 group O-derived proteins
 CC from cell cultures or biological tissues. The monoclonal antibodies can
 CC also be used for generating chimeric antibodies for therapeutic use.
 CC Different synthetic, recombinant or purified antibodies which identify
 CC different epitopes of HIV antigens can be used in combination in assay to
 CC diagnose, evaluate, or prognosticate HIV disease condition. The
 CC monoclonal antibodies are also useful for differentiating HIV-1 Group O
 CC antigens from HIV-group M and HIV-2 antigens. Sequences AA77369-77375
 CC represent recombinant HIV-1 group O env antigens encoded by the synthetic
 CC genes AA290280-290286. The recombinant HIV-1 env proteins contain
 CC various deletions relative to the native HAM112 isolate env protein
 CC (AA77376). The recombinant HIV-1 group O antigens were purified and used
 CC to screen hybridoma cultures.
 XX
 SQ Sequence 245 AA;

Very Match 91.3%; Score 116; DB 21; Length 245;
 at Local Similarity 81.8%; Pred. No. 5.3e-08;
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSLMGCRGLVCTSVQNMNET 22
 ||:||||:||||:||||:
 Db 127 LLNLWGCKGRLLICTSVKMMNET 148

Search completed: May 29, 2003, 10:36:20
 Job time : 30.3333 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:36 ; Search time 9.95238 Seconds

(Without alignments)
65.040 Million cell updates/sec

Title: US-09-147-362A-2

Perfect score: 127
Sequence: 1 LLSLMGCRGLVCTSVQNMET 22Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfltest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	91.3	215	2	US-08-912-129A-58
2	116	91.3	245	2	US-08-912-129A-48
3	116	91.3	373	2	US-08-912-129A-52
4	116	91.3	460	2	US-08-912-129A-60
5	116	91.3	490	2	US-08-912-129A-54
6	116	91.3	618	2	US-08-912-129A-61
7	116	91.3	873	2	US-08-912-129A-61
8	115	90.6	37	4	US-08-817-441-94
9	115	90.6	104	4	US-08-817-441-100
10	113	89.0	356	4	US-08-602-713-12
11	113	89.0	356	4	US-08-989-493-12
12	112	88.2	37	4	US-08-817-441-86
13	112	88.2	200	4	US-08-965-056-104
14	111	87.4	23	4	US-08-817-441-30
15	111	87.4	40	3	US-08-894-699-39
16	111	87.4	40	3	US-08-894-699-39
17	111	87.4	40	3	US-08-894-699-39
18	111	87.4	40	3	US-08-894-699-39
19	111	87.4	40	3	US-08-894-699-39
20	110	86.6	40	3	US-08-894-699-41
21	110	86.6	40	3	US-08-894-699-42
22	110	86.6	40	3	US-08-894-699-41
23	110	86.6	40	3	US-08-894-699-41
24	109	85.8	40	3	US-08-894-699-37
25	109	85.8	40	3	US-08-894-699-37
26	108	85.0	40	3	US-08-894-699-40
27	108	85.0	40	4	US-09-444-410-40

28	107	84.3	23	4	US-09-433-428D-68	Sequence 68, Appl
29	107	84.3	33	4	US-09-433-428D-1	Sequence 1, Appl
30	107	84.3	33	4	US-09-433-428D-4	Sequence 15, Appl
31	107	84.3	33	4	US-09-433-428D-15	Sequence 66, Appl
32	107	84.3	42	3	US-08-894-699-66	Sequence 5, Appl
33	107	84.3	42	4	US-09-444-410-66	Sequence 14, Appl
34	106	83.5	33	4	US-09-433-428D-5	Sequence 29, Appl
35	106	83.5	33	4	US-09-433-428D-14	Sequence 101, App
36	106	83.5	33	4	US-08-817-441-101	Sequence 90, Appl
37	106	83.5	37	4	US-08-817-441-7	Sequence 47, Appl
38	106	83.5	37	4	US-08-817-441-90	Sequence 102, App
39	106	83.5	351	4	US-08-817-441-47	Sequence 34, Appl
40	106	83.5	877	4	US-08-817-441-102	Sequence 18, Appl
41	105	82.7	24	4	US-09-433-428D-10	Sequence 19, Appl
42	105	82.7	33	4	US-09-433-428D-18	
43	105	82.7	33	4	US-09-433-428D-18	
44	105	82.7	33	4	US-09-433-428D-19	
45	105	82.7	33	4	US-09-433-428D-19	

ALIGNMENTS

RESULT 1
US-08-912-129A-58
Sequence 58, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITEK, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVAERE, SUSHLI G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Danckerts, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109, US, 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-912-129A-58

Query Match 91.3%; Score 116; DB 2; Length 215;
Best Local Similarity 81.8%; Pred. No. 7.8e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
127 LLSLMGCRGLVCTSVQNMET 148

RESULT 2

US-08-912-129A-48
Sequence 48; Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912.129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckert, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-48

Query Match 91.3%; Score 116; DB 2; Length 245;
Best Local Similarity 81.8%; Pred. No. 9e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
127 LLSLMGCRGLVCTSVQNMET 148

RESULT 3

US-08-912-129A-52
Sequence 52; Application US/08912129A
Patent No. 5922533

GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912.129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckert, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-52

Query Match 91.3%; Score 116; DB 2; Length 373;
Best Local Similarity 81.8%; Pred. No. 1.4e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
127 LLSLMGCRGLVCTSVQNMET 148

RESULT 4

US-08-912-129A-60
Sequence 60; Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckere, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-912-129A-60

Query Match 91.3%; Score 116; DB 2; Length 460;
Best Local Similarity 81.8%; Pred. No. 1.8e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LISTWGCRGLVCTYSVKNNET 22
DB 372 LNTLMGCKRGLVCTYSVKNNET 393

RESULT 5
US-08-912-129A-50
Sequence 50, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997

CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckere, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-50

Query Match 91.3%; Score 116; DB 2; Length 490;
Best Local Similarity 81.8%; Pred. No. 1.9e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LISTWGCRGLVCTYSVKNNET 22
DB 372 LNTLMGCKRGLVCTYSVKNNET 393

RESULT 6
US-08-912-129A-54
Sequence 54, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckere, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-54

Query Match 91.3%; Score 116; DB 2; Length 618;
Best Local Similarity 81.8%; Pred. No. 2.4e-09;

Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLSLMGCRGLVCTSVQNMET 22
Db 372 LLSLMGCRGLVCTSVQNMET 393

RESULT 7

US-08-912-129A-61
Sequence 61, Application US/08912129A
Patent No. 5925133

GENERAL INFORMATION:

APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Dancigers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-912-129A-61

Query Match 91.3%; Score 116; DB 2; Length 873;
Best Local Similarity 81.8%; Pred. No. 3.4e-09;

Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLSLMGCRGLVCTSVQNMET 22

Db 601 LLSLMGCRGLVCTSVQNMET 622

RESULT 8
US-08-817-441-94
Sequence 94, Application US/08817441
Patent No. 6392294

GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
APPLICANT: CLAVEL, FRANCOISE
APPLICANT: BORMAN, ANDREW
APPLICANT: OUILLENT, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: MONTIGNIER, LUC
APPLICANT: DONON DE SAINT-MARTIN, JACQUELINE
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,441
FILING DATE: 11-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-441-94

Query Match 90.6%; Score 115; DB 4; Length 37;
Best Local Similarity 81.8%; Pred. No. 1.7e-10;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSLMGCRGLVCTSVQNMET 22

Db 14 LLSLMGCRGLVCTSVQNMET 35

RESULT 9

US-08-817-441-100
Sequence 100, Application US/08817441

Patent No. 6399294
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
APPLICANT: CLAVEL, FRANCOISE
APPLICANT: BORMAN, ANDREW
APPLICANT: QUILLENT, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: MONTAGNIER, LUC
APPLICANT: DONON DE SAINT-MARTIN, JACQUELINE
APPLICANT: COHEN, JAOUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
TITLE OF INVENTION: SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/817,441
APPLICATION NUMBER: US/08/817,441
FILING DATE: 11-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260, 6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-441-100
Query Match 90.6%; Score 115; DB 4; Length 104;
Best Local Similarity 81.8%; Pred. No. 5, 1e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 LSLMGCRGLVCTYSVQNNET 22
DB 45 LNLWGCRGKALCYTSVQNNET 66
RESULT 10
US-08-602-713-12
Sequence 12, Application US/08602713
Patent No. 5798205
GENERAL INFORMATION:
APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;
APPLICANT: G rtler, Lutz G.; Eberle, Josef; Kapuae, Lazare;
APPLICANT: Zekeng, L opold Achenqui
TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
FILING DATE: (MVP-2901/94)
TITLE OF INVENTION: (MVP-2901/94)

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,713
FILING DATE: 16-FEBRUARY-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 05 262
FILING DATE: 16-FEBRUARY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5798205man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LEDEB 203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
FRAGMENT TYPE: Internal
US-08-602-713-12
Query Match 89.0%; Score 113; DB 1; Length 356;
Best Local Similarity 77.3%; Pred. No. 3, 7e-09;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 LSLMGCRGLVCTYSVQNNET 22
DB 322 LNLWGCKGLICTYSVQNNET 343
RESULT 11
US-08-989-493-12
Sequence 12, Application US/08989493
Patent No. 6162631
GENERAL INFORMATION:
APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;
APPLICANT: G rtler, Lutz G.; Eberle, Josef; Kapuae, Lazare;
APPLICANT: Zekeng, L opold Achenqui
TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
FILING DATE: (MVP-2901/94)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,493
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,713
FILING DATE: 16-FEBRUARY-1996
APPLICATION NUMBER: DE 195 05 262
FILING DATE: 16-FEBRUARY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6162631man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LEDER 203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
FRAGMENT TYPE: Internal
8-989-493-12

Query Match 89.0%; Score 113; DB 4; Length 356;
Best Local Similarity 77.3%; Pred. No. 3.7e-09;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCYTSVQNMRT 22
DB 322 LLSLMGCKKGLVCYTSVQNMRT 343

RESULT 12
US-08-817-441-86
Sequence 86, Application US/08817441
Patent No. 6399294
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
APPLICANT: CLAVEL, FRANCOISE
APPLICANT: BORMAN, ANDREW
APPLICANT: GUILLENT, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: MONTAGNIER, LUC
APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE
APPLICANT: COHEN, JAQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
TITLE OF INVENTION: SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,441
FILING DATE: 11-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-441-86

Query Match 88.2%; Score 112; DB 4; Length 37;
Best Local Similarity 81.8%; Pred. No. 4.7e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCYTSVQNMRT 22
DB 14 LLSLMGCKKGLVCYTSVQNMRT 35

RESULT 13
US-08-965-056-104
Sequence 104, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-NOV-6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-965-056-104

Query Match 88.2%; Score 112; DB 4; Length 200;
Best Local Similarity 81.8%; Pred. No. 2.8e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCYTSVQNMRT 22

Db 126 LLSLMGCKGRKLVCTTSVQNMRT 147

RESULT 14

US-08-817-441-30
Sequence 30, Application US/08817441

Patent No. 6399294

GENERAL INFORMATION:

APPLICANT: CHARNEAU, PIERRE

APPLICANT: CLAVEL, FRANCOISE

APPLICANT: BORMAN, ANDREW

APPLICANT: OUILLENT, CAROLINE

APPLICANT: GUETARD, DENISE

APPLICANT: MONTAGNIER, LUC

APPLICANT: DONOUD DE SAINT-MARTIN, JACQUELINE

APPLICANT: COHEN, JACQUES

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR

TITLE OF INVENTION: SUBTYPE) ANTIGENS

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &

ADDRESS: 1300 I Street, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/817.441

FILING DATE: 11-JUL-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR 95/01391

FILING DATE: 20-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9412554

FILING DATE: 20-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9502526

FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03260.6005-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-817-441-30

Query Match 87.4%; Score 111; DB 4; Length 23;

Best Local Similarity 81.0%; Pred. No. 4e-10;

Matches 17; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLSLMGCKGRKLVCTTSVQNMRT 22

Db 1 LLSLMGCKGRKLVCTTSVQNMRT 21

RESULT 15

US-08-894-699-39
Sequence 39, Application US/08894699

Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SATOR

APPLICANT: LOUSSEST-AJAKA, IBITISSAM

APPLICANT: LY, THOAI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

TITLE OF INVENTION: VIRUSES, AND USES THEREOF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894.699

FILING DATE: 01-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294

FILING DATE: 26-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-894-699-39

Query Match 87.4%; Score 111; DB 3; Length 40;

Best Local Similarity 81.8%; Pred. No. 7.2e-10;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSLMGCKGRKLVCTTSVQNMRT 22

Db 19 LLSLMGCKGRKLVCTTSVQNMRT 40

Search completed: May 29, 2003, 10:41:27
Job time: 10.9524 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:39:21 ; Search time 19.0317 Seconds

(Without alignments)
117.011 Million cell updates/sec

Title: US-09-147-362A-2

Perfect score: 127
Sequence: 1 LLSLMGCRGLVCTSVQNMNET 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PC7_NEM_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEM_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PC7_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	91.3	215	1 US-08-911-824-58	Sequence 58, Appl
2	116	91.3	245	1 US-08-911-824-48	Sequence 48, Appl
3	116	91.3	281	1 US-08-911-824-120	Sequence 120, Appl
4	116	91.3	373	1 US-08-911-824-52	Sequence 52, Appl
5	116	91.3	460	1 US-08-911-824-60	Sequence 60, Appl
6	116	91.3	488	1 US-08-911-824-95	Sequence 95, Appl
7	116	91.3	490	1 US-08-911-824-50	Sequence 50, Appl
8	116	91.3	526	1 US-08-911-824-97	Sequence 97, Appl
9	116	91.3	618	1 US-08-911-824-54	Sequence 54, Appl
10	116	91.3	706	1 US-08-911-824-93	Sequence 93, Appl
11	116	91.3	726	1 US-08-911-824-91	Sequence 91, Appl
12	116	91.3	873	1 US-08-911-824-61	Sequence 61, Appl
13	115	90.6	37	9 US-10-026-741-94	Sequence 94, Appl
14	115	90.6	104	9 US-10-026-741-100	Sequence 100, Appl
15	112	88.2	37	9 US-10-026-741-86	Sequence 86, Appl
16	112	88.2	200	10 US-09-854-816-104	Sequence 104, Appl
17	111	87.4	32	9 US-10-026-741-30	Sequence 30, Appl
18	106	83.5	35	9 US-10-026-741-101	Sequence 101, Appl
19	106	83.5	37	9 US-10-026-741-7	Sequence 7, Appl

20	106	83.5	37	9 US-10-026-741-90	Sequence 90, Appl
21	106	83.5	351	9 US-10-026-741-47	Sequence 47, Appl
22	106	83.5	877	9 US-10-026-741-102	Sequence 102, Appl
23	105	82.7	24	9 US-10-026-741-34	Sequence 34, Appl
24	104	81.9	37	9 US-10-026-741-88	Sequence 88, Appl
25	102	80.3	213	10 US-09-854-816-103	Sequence 103, Appl
26	99	78.0	23	9 US-09-388-847-4	Sequence 4, Appl
27	99	78.0	23	12 US-10-000-321-2	Sequence 2, Appl
28	99	78.0	35	9 US-09-886-156-62	Sequence 62, Appl
29	99	78.0	35	9 US-09-886-150-62	Sequence 62, Appl
30	99	78.0	35	9 US-09-886-149-62	Sequence 62, Appl
31	99	78.0	35	9 US-09-886-159-62	Sequence 62, Appl
32	99	78.0	146	12 US-10-000-321-10	Sequence 10, Appl
33	99	78.0	204	10 US-09-854-816-105	Sequence 105, Appl
34	99	78.0	351	9 US-09-886-156-46	Sequence 46, Appl
35	99	78.0	351	9 US-09-886-150-46	Sequence 46, Appl
36	99	78.0	351	9 US-09-886-149-46	Sequence 46, Appl
37	99	78.0	351	9 US-09-886-159-46	Sequence 46, Appl
38	89	70.1	37	9 US-10-026-741-84	Sequence 84, Appl
39	89	70.1	204	10 US-09-854-816-106	Sequence 106, Appl
40	89	70.1	268	10 US-09-854-816-39	Sequence 39, Appl
41	86	67.7	198	10 US-09-854-816-78	Sequence 78, Appl
42	84	66.1	37	9 US-10-026-741-82	Sequence 82, Appl
43	84	66.1	198	10 US-09-854-816-77	Sequence 77, Appl
44	84	66.1	198	10 US-09-854-816-80	Sequence 80, Appl
45	84	66.1	198	10 US-09-854-816-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-08-911-824-58
Sequence 58, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackert, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165-US-01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 58
LENGTH: 215
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-8P.
US-08-911-824-58
Query Match 91.3%; Score 116; DB 1; Length 215;
Best Local Similarity 81.8%; Pred. No. 4e-09;
Matches 18; Conservative 4; Mismatches 0; Gaps 0;
QY 1 LLSLMGCRGLVCTSVQNMNET 22
DB 127 LLSLMGCRGLVCTSVQNMNET 148
RESULT 2
US-08-911-824-48
Sequence 48, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories

```

; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 245
; TYPE: PRP
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-9PL
8-911-824-48

```

```

Query Match          91.3%; Score 116; DB 1; Length 245;
Best Local Similarity 81.8%; Pred. No. 4.6e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LSLMGCGRGLVCTSVOMNET 22
Db 127 LNLWGCCKRGLICTSVKNET 148

```

```

RESULT 3
US-08-911-824-120
; Sequence 120, Application US/08911824
; Publication No. US20030004333A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 281
; TYPE: PRP
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-15PL
US-08-911-824-120

```

```

Query Match          91.3%; Score 116; DB 1; Length 281;
Best Local Similarity 81.8%; Pred. No. 5.2e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LSLMGCGRGLVCTSVOMNET 22
Db 127 LNLWGCCKRGLICTSVKNET 148

```

```

RESULT 4
US-08-911-824-52
; Sequence 52, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.

```

```

; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 373
; TYPE: PRP
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-11PL
US-08-911-824-52

```

```

Query Match          91.3%; Score 116; DB 1; Length 373;
Best Local Similarity 81.8%; Pred. No. 6.8e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LSLMGCGRGLVCTSVOMNET 22
Db 127 LNLWGCCKRGLICTSVKNET 148

```

```

RESULT 5
US-08-911-824-60
; Sequence 60, Application US/08911824
; Publication No. US20030004333A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 460
; TYPE: PRP
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-8CKS
US-08-911-824-60

```

```

Query Match          91.3%; Score 116; DB 1; Length 460;
Best Local Similarity 81.8%; Pred. No. 8.2e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LSLMGCGRGLVCTSVOMNET 22
Db 372 LNLWGCCKRGLICTSVKNET 393

```

```

RESULT 6
US-08-911-824-95
; Sequence 95, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie

```


APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 95
LENGTH: 488
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-14PL
US-08-911-824-95

Query Match 91.3%; Score 116; DB 1; Length 488;
Best Local Similarity 81.8%; Pred. No. 8.7e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
||:||||:||||:||||:
Db 127 LNLWGCGRGLICTSVKMNET 148

RESULT 7
US-08-911-824-50
Sequence 50, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 490
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-9CKS
US-08-911-824-50

Query Match 91.3%; Score 116; DB 1; Length 490;
Best Local Similarity 81.8%; Pred. No. 8.7e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
||:||||:||||:||||:
Db 372 LNLWGCGRGLICTSVKMNET 393

RESULT 8
US-08-911-824-97
Sequence 97, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.

APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 97
LENGTH: 526
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-15CKS
US-08-911-824-97

Query Match 91.3%; Score 116; DB 1; Length 526;
Best Local Similarity 81.8%; Pred. No. 9.3e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
||:||||:||||:||||:
Db 372 LNLWGCGRGLICTSVKMNET 393

RESULT 9
US-08-911-824-54
Sequence 54, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 618
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-11CKS
US-08-911-824-54

Query Match 91.3%; Score 116; DB 1; Length 618;
Best Local Similarity 81.8%; Pred. No. 1.1e-08;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMET 22
||:||||:||||:||||:
Db 372 LNLWGCGRGLICTSVKMNET 393

RESULT 10
US-08-911-824-93
Sequence 93, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.

```

; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 706
; TYPE: PRP
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-13CKS
US-08-911-824-93

Query Match          91.3%; Score 116; DB 1; Length 706;
Best Local Similarity 81.8%; Pred.No. 1.2e-08;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LISTMCGRGLVCTSVQNNET 22
||:||||:||||:||||:||||:
Db 618 LILNMGCKGRILICTSVKNNET 639

RESULT 11
US-08-911-824-91
; Sequence 91, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 736
; TYPE: PRP
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-12CKS
US-08-911-824-91

Query Match          91.3%; Score 116; DB 1; Length 736;
Best Local Similarity 81.8%; Pred.No. 1.3e-08;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LISTMCGRGLVCTSVQNNET 22
||:||||:||||:||||:||||:
Db 618 LILNMGCKGRILICTSVKNNET 639

RESULT 12
US-08-911-824-61
; Sequence 61, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
```

```

; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 873
; TYPE: PRP
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: HIV-1 Group O isolate HAM112
US-08-911-824-61

Query Match          91.3%; Score 116; DB 1; Length 873;
Best Local Similarity 81.8%; Pred.No. 1.5e-08;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LISTMCGRGLVCTSVQNNET 22
||:||||:||||:||||:||||:
Db 601 LILNMGCKGRILICTSVKNNET 622

RESULT 13
US-10-026-741-94
; Sequence 94, Application US/10026741
; Publication No. US20030049604A1
; GENERAL INFORMATION:
; APPLICANT: CHARNEAU, PIERRE
; APPLICANT: CLAVEL, FRANCOISE
; APPLICANT: BORMAN, ANDREW
; APPLICANT: QUILLENT, CAROLINE
; APPLICANT: GUETARD, DENISE
; APPLICANT: MONTAGNIER, IUC
; APPLICANT: DONON, DE SAINT-MARTIN, JACQUELINE
; APPLICANT: COHEN, JAOUES
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
; SUBTYPE) ANTIGENS
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/026,741
; FILING DATE: 27-Dec-2001
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/817,441
; FILING DATE: 31-AUG-1998
; APPLICATION NUMBER: PCT/FR 95/01391
; FILING DATE: 20-OCT-1995
; APPLICATION NUMBER: FR 9412554
; FILING DATE: 20-OCT-1994
; APPLICATION NUMBER: FR 9502526
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03260,6005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
```

INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-10-026-741-94

Query Match
Best Local Similarity 81.8%; Pred. No. 1.1e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LSLMGCRGLVCTSVQNNET 22
||:|||||:|||||
14 LNLWGCRGKAICTSVQNNET 35

RESULT 14
US-026-741-100
Sequence 100, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
QUILLIENT, CAROLINE
GUETARD, DENISE
MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQUELINE
COHEN, JACQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-026-741-100

Query Match
Best Local Similarity 89.6%; Score 115; DB 9; Length 104;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LSLMGCRGLVCTSVQNNET 22
||:|||||:|||||
45 LNLWGCRGKAICTSVQNNET 66

RESULT 15
US-10-026-741-86
Sequence 86, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
QUILLIENT, CAROLINE
GUETARD, DENISE
MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQUELINE
COHEN, JACQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-026-741-86

Query Match
Best Local Similarity 88.2%; Score 112; DB 9; Length 37;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LLSIMGCGRRLVCYTSVQNNET 22
Db 14 LLSIMGCGKGLVCYTSVKNNRT 35

Search completed: May 29, 2003, 11:03:56
Job time : 20.0317 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:06 ; Search time 10.8254 Seconds
(without alignments)
195.370 Million cell updates/sec

Title: US-09-147-362A-2

Perfect score: 127

Sequence: 1 LLSLMGCRGRLLVCTYSVQNMNET 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	90.6	104	2	GP41 ENV protein -
2	112	88.2	863	2	gag polyprotein -
3	106	83.5	877	2	env polyprotein p
4	89	70.1	854	1	env polyprotein pr
5	86	67.7	357	2	env polyprotein g
6	85	66.9	358	2	env polyprotein g
7	85	66.9	358	2	env polyprotein g
8	85	66.9	358	2	env polyprotein g
9	84	66.1	443	2	env polyprotein p
10	84	66.1	853	2	env polyprotein p
11	84	66.1	853	2	env polyprotein p
12	83	65.4	357	2	env polyprotein g
13	83	65.4	357	2	env polyprotein g
14	83	65.4	357	2	env polyprotein g
15	83	65.4	357	2	env polyprotein g
16	83	65.4	357	2	env polyprotein g
17	83	65.4	357	2	env polyprotein g
18	83	65.4	357	2	env polyprotein g
19	83	65.4	357	2	env polyprotein g
20	83	65.4	357	2	env polyprotein g
21	83	65.4	357	2	env polyprotein g
22	83	65.4	357	2	env polyprotein g
23	83	65.4	357	2	env polyprotein g
24	83	65.4	357	2	env polyprotein g
25	83	65.4	357	2	env polyprotein g
26	83	65.4	357	2	env polyprotein g
27	83	65.4	357	2	env polyprotein g
28	83	65.4	357	2	env polyprotein g
29	83	65.4	357	2	env polyprotein g

30	83	65.4	861	1	VCLJLV	env polyprotein pr
31	83	65.4	861	1	VCLJSC	env polyprotein pr
32	81	63.8	856	1	A44963	env polyprotein pr
33	81	63.8	859	1	VCLJMN	env polyprotein pr
34	81	63.8	868	1	VCLJH4	env polyprotein pr
35	80	63.0	846	1	VCLJND	env polyprotein pr
36	77	60.6	729	1	VCLJKB	env polyprotein pr
37	77	60.6	861	1	VCLJKB	env polyprotein pr
38	76	59.8	766	2	S28084	env polyprotein -
39	76	59.8	851	2	S33985	env polyprotein -
40	74	58.3	859	2	T01672	env polyprotein -
41	72.5	57.1	855	2	A45713	env polyprotein -
42	68.5	53.9	859	1	VCLJST	env polyprotein pr
43	68.5	53.9	859	2	S24571	env polyprotein -
44	68.5	53.9	855	2	S04322	env polyprotein -
45	68.5	53.9	886	2	T11555	env protein - simi

ALIGNMENTS

RESULT 1
GP41 ENV protein - human immunodeficiency virus type 1 (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C/Accession: S52930
R/Cohen, J.H.M.; Guetard, D.; Philbert, F.; Chameret, S.; Tabary, T.; Montagnier, L.; de
submitted to the EMBL Data Library, January 1995
A/Description: A novel HIV-1 strain illustrates the diversity of the O group.
A/Reference number: S52929
A/Accession: S52930
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-104 <COH>
A/Cross-references: EMBL:X84328; NID:G695526; PID:CA59066.1; PID:G695527
C/Superfamily: type E retrovirus env polyprotein

Query Match 90.6%; Score 115; DB 2; Length 104;
Best Local Similarity 81.8%; Pred. No. 1.3e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSLMGCRGRLLVCTYSVQNMNET 22
Db 45 LLSLMGCRGRLLVCTYSVQNMNET 66

RESULT 2

A53034
gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C/Accession: A53034
R/Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groen,
J.; Virel, G.; 1586-1596, 1994
A/Title: Genomic cloning and complete sequence analysis of a highly divergent African hu
A/Reference number: A53034; MUID:9419849; PMID:8107220
A/Accession: A53034
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-863 <VAN>
A/Cross-references: GB:L02587
C/Superfamily: type B retrovirus env polyprotein
C/Keywords: polyprotein

Query Match 88.2%; Score 112; DB 2; Length 863;
Best Local Similarity 81.8%; Pred. No. 2.2e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSLMGCRGRLLVCTYSVQNMNET 22
Db 594 LLSLMGCRGRLLVCTYSVQNMNET 615

RESULT 3

envelope protein precursor - human immunodeficiency virus type 1 (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
 C:Accession: S49197
 R:Charneau, P.; Bormar, A.M.; Oullent, C.; Guetard, D.; Chamaret, S.; Cohen, J.; Remy,
 submitted to the EMBL Data Library, July 1994
 A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defn
 A:Reference number: S49197
 A:Accession: S49197
 A:Molecule type: DNA
 A:Residues: 1-877 <CHA>
 A:CiCross-references: EMBL:X80020; NID:G510516; PIDN:CA56323.1; PID:G510517
 A:Experimental source: Isolate VAU
 C:Superfamily: type B retrovirus env polyprotein
 C:Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein
 F.1-30/Domains: signal sequence #status predicted <SIG>
 F.1-53/Product: coat protein gp120 #status predicted <CP1>
 F.54-877/Product: coat protein gp1 #status predicted <CP2>
 F.898-716/Domains: transmembrane #status predicted <TMN>
 F.759, 88, 139, 146, 159, 184, 188, 198, 230, 235, 242, 263, 270, 277, 292, 302, 333, 345, 357, 367, 396, 404, 415, 579, 586, 139, 146, 159, 184, 188, 198, 230, 235, 242, 263, 270, 277, 292, 302, 333, 345, 357, 367, 396, 404, 415

\$21990

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 20
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21990; S70423
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
A:Reference number: S21990
A:Accession: S21990
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61357; NID:G60175; PIDD:CAA43626.1; PID:G60176
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332, 'X', 334-357 <STE2>
A:Cross-references: EMBL:X61357; NID:G60175; PIDD:CAA43626.1; PID:G60176
C:Superfamily: type E retrovirus env polyprotein

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
 C/Accession: S22000
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Haecke, W.
 Submitted to the EMBL Data Library, July 1991
 A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
 A/Reference number: S21990
 A/Accession: S22000
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-358 <STR>
 A/Cross-references: EMBL:X61351
 C/Superfamily: type E retrovirus env polypotein

Query Match 66.9%; Score 85; DB 2; Length 358;
 Best Local Similarity 65.0%; Pred. No. 8.4e-05;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

1 LLSLMGCRGLVCTYSVQMN 20
 ||:|||||:|||||:
 94 LLSLMGCRGLVCTYSVQMN 113

RESULT 8
 S70417
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Variety: patient 3B
 C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
 C/Accession: S70417
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb
 A/Reference number: S70417; MUID:92144209; PMID:1736940
 A/Accession: S70417
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-358 <STR>
 A/Cross-references: EMBL:X61351; NID:G60184; PIDN:CAA43614.1; PID:G60185
 C/Superfamily: type E retrovirus env polypotein

Query Match 66.9%; Score 85; DB 2; Length 358;
 Best Local Similarity 65.0%; Pred. No. 8.4e-05;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

1 LLSLMGCRGLVCTYSVQMN 20
 ||:|||||:|||||:
 94 LLSLMGCRGLVCTYSVQMN 113

LT 9
 C41621
 env polypotein P - human immunodeficiency virus type 1 (fragment)
 N/Alternate names: coat polypotein
 N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
 C/Accession: C41621
 R/Burger, H.; Weiser, B.; Flaherty, K.; Galla, J.; Nguyen, P.N.; Gibbs, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 11236-11240, 1991
 A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A/Reference number: A41621; MUID:92107924; PMID:1763038
 A/Accession: C41621
 A/Molecule type: DNA
 A/Residues: 1-443 <STR>
 A/Cross-references: GB:M77230; NID:G328631; PIDN:AA803792.1; PID:G555015
 A/Note: this virus was isolated from the mother's sexual partner
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polypotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypot
 F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:424-443/Domain: transmembrane #status predicted <TMN>
 F:9,23,36,48,78,101,107,131,137,143,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 66.1%; Score 84; DB 2; Length 443;
 Best Local Similarity 54.5%; Pred. No. 0.00014;
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 LLSLMGCRGLVCTYSVQNET 22
 ||:|||||:|||||:
 332 LLSLMGCRGLVCTYSVQNET 353

RESULT 10
 S54384
 envelope polypotein - human immunodeficiency virus type 1
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
 C/Accession: S54384
 R/Theodore, T.; Buckler-White, A.J.
 submitted to the EMBL Data Library, July 1989
 A/Reference number: S54377
 A/Accession: S54384
 A/Status: preliminary
 A/Molecule type: genomic RNA
 A/Residues: 1-853 <TR>
 A/Cross-references: EMBL:M2639; NID:G329377; PIDN:AAA45370.1; PID:G329385
 C/Superfamily: type E retrovirus env polypotein
 C/Keywords: polypotein

Query Match 66.1%; Score 84; DB 2; Length 853;
 Best Local Similarity 54.5%; Pred. No. 0.00025;
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 LLSLMGCRGLVCTYSVQNET 22
 ||:|||||:|||||:
 589 LLSLMGCRGLVCTYSVQNET 610

RESULT 11
 VCLJZR
 env polypotein precursor - human immunodeficiency virus Zr-6
 N/Alternate names: coat polypotein
 C/Species: human immunodeficiency virus Zr-6
 C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
 C/Accession: D26192
 R/Srinivasan, A.; Anand, R.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
 Gene 52, 71-82, 1987
 A/Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotide
 A/Reference number: A26192; MUID:87248097; PMID:3036660
 A/Accession: D26192
 A/Molecule type: DNA
 A/Residues: 1-855 <STR>
 A/Cross-references: GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45380.1; PID:G329403
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polypotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypot
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-855/Product: env polypotein #status predicted <MNT>
 F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
 F:501-855/Product: transmembrane glycoprotein #status predicted <TMN>
 F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match 66.1%; Score 84; DB 1; Length 855;
 Best Local Similarity 54.5%; Pred. No. 0.00025;
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 LLSLMGCRGLVCTYSVQNET 22
 ||:|||||:|||||:
 591 LLSLMGCRGLVCTYSVQNET 612

RESULT 12

S22006
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S70420, S22006
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70420
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A:Cross-references: EMBL:X61354; NID:G60190; PIDN:CAA43620.1; PID:G60191
 A:Experimental source: patient L
 A>Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 65.4%; Score 83; DB 2; Length 357;
 Best Local Similarity 60.0%; Pred. No. 0.00016;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LLSLMGCRGLVCTSVQWN 20
 ||:|||||:|:|:|
 Db 93 LLSLMGCRGLVCTSVQWN 112

RESULT 13
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Variety: isolate 278
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C:Accession: S21994, S70421
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR
 A:Reference number: S21994
 A:Accession: S21994
 A:Molecule type: DNA
 A:Residues: 1-357 <STB1>
 A:Cross-references: EMBL:X61355; NID:G60179; PIDN:CAA43622.1; PID:G60180
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70421
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STB2>
 A:Cross-references: EMBL:X61355; NID:G60179
 C:Superfamily: type E retrovirus env polyprotein

Query Match 65.4%; Score 83; DB 2; Length 357;
 Best Local Similarity 60.0%; Pred. No. 0.00016;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LLSLMGCRGLVCTSVQWN 20
 ||:|||||:|:|:|
 Db 93 LLSLMGCRGLVCTSVQWN 112

RESULT 14
 S22004
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Variety: isolate 4B
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C:Accession: S22004, S70419
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
 A:Reference number: S21990

A:Accession: S22004
 A:Molecule type: DNA
 A:Residues: 1-357 <STB1>
 A:Cross-references: EMBL:X61353; NID:G60188; PIDN:CAA43618.1; PID:G60189
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70419
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-292, 'X', 294-357 <STB2>
 A:Cross-references: EMBL:X61353; NID:G60188
 C:Superfamily: type E retrovirus env polyprotein

Query Match 65.4%; Score 83; DB 2; Length 357;
 Best Local Similarity 60.0%; Pred. No. 0.00016;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LLSLMGCRGLVCTSVQWN 20
 ||:|||||:|:|:|
 Db 93 LLSLMGCRGLVCTSVQWN 112

RESULT 15
 S21996
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S70422, S21996
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70422
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A:Cross-references: EMBL:X61356; NID:G60181; PIDN:CAA43624.1; PID:G1067129
 A:Experimental source: patient 27L
 A>Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 65.4%; Score 83; DB 2; Length 357;
 Best Local Similarity 60.0%; Pred. No. 0.00016;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LLSLMGCRGLVCTSVQWN 20
 ||:|||||:|:~|:|
 Db 93 LLSLMGCRGLVCTSVQWN 112

Search completed: May 29, 2003, 10:40:23
 Job time: 10.8254 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:31:50; Search time 5.4127 Seconds
(without alignments)
168.581 Million cell updates/sec

Title: US-09-147-362A-2

Sequence: 1 LLSLMGCRGLVCTSVQNMET 22

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	70.1	854	1 ENV_SIVC2	P17281 chimpanzee
2	84	66.1	853	1 ENV_HV122	P14877 human immun
3	84	66.1	855	1 ENV_HV126	P04580 human immun
4	83	65.4	843	1 ENV_HV122	P35961 human immun
5	83	65.4	847	1 ENV_HV121	P19550 human immun
6	83	65.4	847	1 ENV_HV122	P05880 human immun
7	83	65.4	851	1 ENV_HV128	P04582 human immun
8	83	65.4	852	1 ENV_HV128	P12488 human immun
9	83	65.4	852	1 ENV_HV128	P19549 human immun
10	83	65.4	853	1 ENV_HV128	P19551 human immun
11	83	65.4	855	1 ENV_HV128	P03378 human immun
12	83	65.4	855	1 ENV_HV128	P20888 human immun
13	83	65.4	856	1 ENV_HV128	P03378 human immun
14	83	65.4	856	1 ENV_HV128	P04578 human immun
15	83	65.4	856	1 ENV_HV128	P03378 human immun
16	83	65.4	856	1 ENV_HV128	P03378 human immun
17	83	65.4	856	1 ENV_HV128	P03378 human immun
18	83	65.4	856	1 ENV_HV128	P03378 human immun
19	83	65.4	856	1 ENV_HV128	P03378 human immun
20	83	65.4	856	1 ENV_HV128	P03378 human immun
21	83	65.4	856	1 ENV_HV128	P03378 human immun
22	83	65.4	856	1 ENV_HV128	P03378 human immun
23	83	65.4	856	1 ENV_HV128	P03378 human immun
24	83	65.4	856	1 ENV_HV128	P03378 human immun
25	83	65.4	856	1 ENV_HV128	P03378 human immun
26	83	65.4	856	1 ENV_HV128	P03378 human immun
27	83	65.4	856	1 ENV_HV128	P03378 human immun
28	83	65.4	856	1 ENV_HV128	P03378 human immun
29	83	65.4	856	1 ENV_HV128	P03378 human immun
30	83	65.4	856	1 ENV_HV128	P03378 human immun
31	83	65.4	856	1 ENV_HV128	P03378 human immun
32	83	65.4	856	1 ENV_HV128	P03378 human immun
33	83	65.4	856	1 ENV_HV128	P03378 human immun

34	68.5	53.9	859	1 ENV_HV2D2	P15831 human immun
35	68.5	53.9	885	1 ENV_SIVS4	P12492 simian immu
36	67	52.8	857	1 ENV_HV2XR	Q74126 human immu
37	65.5	51.6	712	1 ENV_HV2S2	P32536 human immu
38	65.5	51.6	846	1 ENV_HV2SB	P12449 human immu
39	65.5	51.6	859	1 ENV_HV2ST	P20872 human immu
40	65	51.2	882	1 ENV_SIVM1	P05885 simian immu
41	64.5	50.8	859	1 ENV_HV2CA	P24105 human immu
42	64	50.4	380	1 ENV_SIVM2	P08810 simian immu
43	64	50.4	865	1 ENV_SIVM2	P05886 simian immu
44	64	50.4	881	1 ENV_SIVM1	P05884 simian immu
45	63	49.6	851	1 ENV_HV2D1	P17755 human immu

ALIGNMENTS

RESULT 1	ENV_SIVC2	STANDARD;	PRT;	854 AA.
ID	ENV_SIVC2			
AC	P17281;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]			
GN	ENV.			
OS	Chimpanzee immunodeficiency virus (SIVcpz) (CIV).			
OC	Viruses; Retroviruses; Retroviridae; Lentiviruses.			
OX	NCBI_TaxID=11723;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=90259077; PubMed=2188136;			
RX	Huet T., Cheynier R., Meyers A., Roelants G., Main-Hobson S.,			
RT	"Genetic organization of a chimpanzee lentivirus related to HIV-1."			
RL	Nature 345:356-359(1990)			
CC	-I- STIMULATORY: STRONG, WITH HIV-1 ENV POLYPROTEIN.			
CC	-----			
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CC	-----			
DR	EMBL: X52154; CA36407.1; -			
DR	P17: S09990; VCLJST			
DR	HIV; X52154; ENVSCP2.			
DR	InterPro: IPR000328; ENV_GP41.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	CHAIN	1	30	
FT	CHAIN	501	500	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	TRANSMEM	501	854	TRANSMEMBRANE GLYCOPROTEIN.
FT	TRANSMEM	501	517	POTENTIAL.
FT	TRANSMEM	675	693	POTENTIAL.
FT	TRANSMEM	805	821	POTENTIAL.
FT	CARBOHYD	134	140	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	140	143	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	143	143	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	143	154	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	260	260	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	267	267	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	299	299	N-LINKED (GLCNAC. . .)

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FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 854 AA; 95803 MW; 2E249AFAD4FD9B3 CRC64;

Query Match
Best Local Similarity 70.1%; Score 89; DB 1; Length 854;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

1 ILISMGCRRLVCYTSVQNMET 22
: ||||| : ||||| :
582 ILGLWCGSGKAVCTTVPNMNS 603

RESULT 2
ENV_HV122 STANDARD; PRT; 853 AA.
ID ENV_HV122
AC P12487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11683;
RX [1]
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
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-----
CC EMBL; M22639; AAA45370.1; -
CC DR HIV; M22639; ENV62226.
CC DR InterPro; IPR000328; ENV GP41.
CC DR InterPro; IPR000777; GP120.
CC DR Pfam; PF00516; GP120; 1.
CC DR Pfam; PF00517; GP41; 1.
CC KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 853 AA; 97043 MW; 849B0B8CBAFF7008 CRC64;

Query Match
Best Local Similarity 66.1%; Score 84; DB 1; Length 853;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 ILISMGCRRLVCYTSVQNMET 22
: ||||| : ||||| :
589 ILGLWCGSGKLCITTVPMNS 610

RESULT 3
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11708;
RX [1]
RA Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from
RT Zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene."
RL Gene 52:71-82(1987).
-----
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-----
CC EMBL; X03458; AAA45380.1; -
CC DR PIR; D26192; VCLJZR.

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DR HIV; K03458; ENV526.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120, 1.
 DR Pfam: PF00517; GP41, 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 510
 FT CHAIN 511 855
 FT DISULFID 53 73
 FT DISULFID 118 207
 FT DISULFID 125 198
 FT DISULFID 130 155
 FT DISULFID 220 249
 FT DISULFID 230 241
 FT DISULFID 298 332
 FT DISULFID 378 444
 FT DISULFID 385 417
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 140 140
 FT CARBOHYD 145 145
 FT CARBOHYD 154 154
 FT CARBOHYD 158 158
 FT CARBOHYD 186 186
 FT CARBOHYD 189 189
 FT CARBOHYD 199 199
 FT CARBOHYD 236 236
 FT CARBOHYD 243 243
 FT CARBOHYD 264 264
 FT CARBOHYD 278 278
 FT CARBOHYD 291 291
 FT CARBOHYD 297 297
 FT CARBOHYD 333 333
 FT CARBOHYD 340 340
 FT CARBOHYD 355 355
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 398 398
 FT CARBOHYD 404 404
 FT CARBOHYD 443 443
 FT CARBOHYD 447 447
 FT CARBOHYD 460 460
 FT CARBOHYD 461 461
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 FT CARBOHYD 610 610
 FT CARBOHYD 615 615
 FT CARBOHYD 624 624
 FT CARBOHYD 636 636
 FT CARBOHYD 673 673
 FT CARBOHYD 855 AA; 96971 MW; 384D3DE239C3457 CRC64;
 SQ SEQUENCE

Query Match 66.1%; Score 84; DB 1; Length 855;
 Best Local Similarity 54.5%; Pred. No. 2.6e-05;
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSIMCGRGLVCTYSVQNET 22
 DB 591 LLSIMCGRGLVCTYSVQNET 612

RESULT 4
 ENV_HV1Y2 STANDARD; PRT: 843 AA.
 AC P35961;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).

OC viruses; Retroviral viruses; Retroviridae; Lentivirus.
 RN NCBI_TaxID=36377;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93021387; PubMed=1404605;
 RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
 Shaw G.M.;
 RT "Complete nucleotide sequence, genome organization, and biological
 properties of human immunodeficiency virus type 1 in vivo: evidence
 for limited defectiveness and complementation.";
 RT J. Virol. 66:6587-6600(1992).
 CC -----
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 CC -----
 CC EMBL; M93258; -; NOT_ANNOTATED_CDS.
 DR PIR; H44001; H44001.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120, 1.
 DR Pfam; PF00517; GP41, 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 489
 FT CHAIN 490 843
 FT TRANSMEM 738 755
 FT DISULFID 53 73
 FT DISULFID 118 201
 FT DISULFID 125 192
 FT DISULFID 130 155
 FT DISULFID 214 243
 FT DISULFID 224 235
 FT DISULFID 292 326
 FT DISULFID 373 432
 FT DISULFID 380 405
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 135 135
 FT CARBOHYD 138 138
 FT CARBOHYD 154 154
 FT CARBOHYD 158 158
 FT CARBOHYD 184 184
 FT CARBOHYD 193 193
 FT CARBOHYD 230 230
 FT CARBOHYD 237 237
 FT CARBOHYD 258 258
 FT CARBOHYD 272 272
 FT CARBOHYD 285 285
 FT CARBOHYD 291 291
 FT CARBOHYD 297 297
 FT CARBOHYD 327 327
 FT CARBOHYD 351 351
 FT CARBOHYD 381 381
 FT CARBOHYD 389 389
 FT CARBOHYD 395 395
 FT CARBOHYD 400 400
 FT CARBOHYD 435 435
 FT CARBOHYD 450 450
 FT CARBOHYD 598 598
 FT CARBOHYD 603 603
 FT CARBOHYD 612 612
 FT CARBOHYD 624 624
 FT CARBOHYD 803 803
 FT CARBOHYD 843 AA; 95648 MW; C69DFD971C918B71 CRC64;
 SQ SEQUENCE

Query Match 65.4%; Score 83; DB 1; Length 843;
 Best Local Similarity 60.0%; Pred. No. 3.7e-05;

Matches	12;	Conservative	4;	Mismatches	4;	Indels	0;	Gaps	0
QY	1	LSLWMCGRGLVYTSYVNN	20						
Db	579	LGIGWCGSKLICTTTPWN	598						
RESULT 5									
ENV_HV1S1	ID	ENV_HV1S1	STANDARD;	PRT;	847	AA.			
AC	PI95E0;								
DT	01-FEB-1991 (Rel. 17, Created)								
DT	01-FEB-1991 (Rel. 17, Last sequence update)								
DT	15-JUL-1999 (Rel. 38, Last annotation update)								
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].								
GN	ENV.								
OS	Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).								
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.								
NCBI_Taxid=11691;	(1)								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=90347835; PubMed=2384920;								
RA	Cheng-Wayer C., Quiroga M., Tung J.W., Dina D., Levy J.;								
RT	"Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation,"								
RL	J. Virol. 64:4390-4398(1990).								
CC	-----								
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CC	-----								
DR	EMBL; M65024; AAA45072.1; -								
DR	HIV; M38428; ENVSESP162.								
DR	InterPro; IPR000328; Env GP41.								
DR	InterPro; IPR000777; GP120.								
DR	Pfam; PF00516; GP120; 1.								
DR	Pfam; PF00517; GP41; 1.								
KV	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;								
KW	Signal.								
FT	SIGNAL	1	29						
FT	CHAIN	30	502						
FT	CHAIN	503	847						
FT	DISULFID	53	73						
FT	DISULFID	118	203						
FT	DISULFID	125	194						
FT	DISULFID	130	155						
FT	DISULFID	216	245						
FT	DISULFID	226	237						
FT	DISULFID	294	328						
FT	DISULFID	374	435						
FT	DISULFID	381	408						
FT	CARBOHYD	87							
FT	CARBOHYD	135	135						
FT	CARBOHYD	154	154						
FT	CARBOHYD	186	186						
FT	CARBOHYD	195	195						
FT	CARBOHYD	232	232						
FT	CARBOHYD	239	239						
FT	CARBOHYD	260	260						
FT	CARBOHYD	274	274						
FT	CARBOHYD	293	293						
FT	CARBOHYD	299	299						
FT	CARBOHYD	329	329						
FT	CARBOHYD	336	336						
FT	CARBOHYD	352	352						
FT	CARBOHYD	382	382						
FT	CARBOHYD	388	388						
FT	CARBOHYD	392	392						
FT	CARBOHYD	392							

FT	CARBOHYD	398	398	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	CARBOHYD	401	401	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	CARBOHYD	438	438	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	CARBOHYD	454	454	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	CARBOHYD	602	602	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	CARBOHYD	607	607	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	CARBOHYD	616	616	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	CARBOHYD	628	628	N-LINKED (GLCNAC . . .) (POTENTIAL) .
SQ	SEQUENCE	847 AA;	96135 MW;	0A01117FD7FFC2AB CRC64;
 Query Match 65.4%; Score 83; DB 1; Length 847; Best Local Similarity 60.0%; Pred. No. 3.7e-05; Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0				
Oy	1 LLSLMGCRGRVCTYSVOVN 20 : : :			
Dd	583 LLGIWGGSGKLCITTAVPWN 602			
 RESULT 6				
ENV_HV1W2	STANDARD;	PRT;	847 AA.	
ID ENV HV1W2	POS680;			
DT	01-NOV-1988	(Rel. 09, Created)		
DT	01-NOV-1988	(Rel. 09, Last sequence update)		
DT	15-JUN-1999	(Rel. 38, Last annotation update)		
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
Gn	ENV.			
OS	Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirae.			
NCBI_TaxID=11705;	[1]			
Rx	SEQUENCE FROM N.A.			
Rx	MEDLINE=86235450; Pubmed=3012778;			
RA	Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D., Salluhuddin S.Z., Mong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;			
RT	"Genetic variation in HTLV-II/LAV over time in patients with AIDS or at risk for AIDS."			
RL	Science 232:1548-1553(1986).			
CC	-I- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.			
CC	-----			
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CC	-----			
DR	EMBL; M12507; AAB12990.1; -			
DR	HIV; M12507; ENVSWMJ2.			
DR	InterPro; IPR000328; Env.GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00517; GP120; 1.			
Kw	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; signal.			
FT	SIGNAL	1	29	
FT	CHAIN	30	501	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	502	847	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	202	BY SIMILARITY.
FT	DISULFID	125	193	BY SIMILARITY.
FT	DISULFID	130	152	BY SIMILARITY.
FT	DISULFID	215	244	BY SIMILARITY.
FT	DISULFID	225	236	BY SIMILARITY.
FT	DISULFID	293	326	BY SIMILARITY.
FT	DISULFID	372	435	BY SIMILARITY.
FT	DISULFID	379	408	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC . . .) (POTENTIAL) .

FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96466 MW; CDIE33D73A58CAE CRC64;

Query Match 65.4%; Score 83; DB 1; Length 847;
Best Local Similarity 60.0%; Pred. No. 3.7e-05;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LLSLMGCRRLVCTYSVQWN 20
||:||||:|:|:|
Db 583 LLSLMGCRRLVCTYSVQWN 602

RESULT 7
ENV_HV1B8 STANDARD; PRT; 851 AA.
AC P04582; (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DB glycoprotein (GP120); Transmembrane glycoprotein (GP41).
GN ENV.

Human immunodeficiency virus type 1 (B8 isolate) (HIV-1).

Viruses; Retroviridae; Retroviridae; Lentivirus.

NCBI_TaxID=11684;

SEQUENCE FROM N.A.

RA MEDLINE=8511123; PubMed=2578615;

RA Ratner L., Haseltine W., Paterson R., Lyak K.J., Starcich B.R.,

RA Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,

RA Baumanster K., Ivanoff L., Petway S.R. Jr., Pearson M.L.,

RA Laubenstein J.A., Papas T.S., Chirgaby J., Chang N.T., Gallo R.C.,

RA Wong-Staal F.; Complete nucleotide sequence of the AIDS virus, HTLV-III.";

RL Nature 313:277-284 (1985).

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CC EMBL, K02011; AAA44661.1; -

DR HIV, K02011; ENV5B8.

DR GlycosubDB, P04582; -

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW Signal.

FT SIGNAL 1 30

FT CHAIN 31 506.

FT CHAIN 507 851

FT DISULFID 54 74

FT DISULFID 119 205

FT DISULFID 126 196

FT DISULFID 131 157

FT DISULFID 218 247

FT DISULFID 228 239

FT DISULFID 296 331

FT DISULFID 378 440

FT DISULFID 385 413

FT CARBOHYD 88

FT CARBOHYD 136

FT CARBOHYD 141 141

FT CARBOHYD 156 156

FT CARBOHYD 160 160

FT CARBOHYD 186 186

FT CARBOHYD 197 197

FT CARBOHYD 230

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 295 295

FT CARBOHYD 301 301

FT CARBOHYD 332 332

FT CARBOHYD 339 339

FT CARBOHYD 356 356

FT CARBOHYD 386 386

FT CARBOHYD 392 392

FT CARBOHYD 401 401

FT CARBOHYD 443 443

FT CARBOHYD 458 458

FT CARBOHYD 606 606

FT CARBOHYD 611 611

FT CARBOHYD 620 620

FT CARBOHYD 632 632

FT CARBOHYD 669 669

FT CARBOHYD 745 745

FT CARBOHYD 811 811

SQ SEQUENCE 851 AA; 96644 MW; D16A3C9085785F1 CRC64;

Query Match 65.4%; Score 83; DB 1; Length 851;
Best Local Similarity 60.0%; Pred. No. 3.7e-05;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LLSLMGCRRLVCTYSVQWN 20
||:||||:|:|:|
Db 587 LLSLMGCRRLVCTYSVQWN 606

ENV_HV1B8 STANDARD; PRT; 852 AA.

AC P12488;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

Human immunodeficiency virus type 1 (BR isolate) (HIV-1).

Viruses; Retroviridae; Retroviridae; Lentivirus.

NCBI_TaxID=11693;

SEQUENCE FROM N.A.

RA MEDLINE=8511123; PubMed=2578615;

RA Ratner L., Haseltine W., Paterson R., Lyak K.J., Starcich B.R.,

RA Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,

RA Baumanster K., Ivanoff L., Petway S.R. Jr., Pearson M.L.,

RA Laubenstein J.A., Papas T.S., Chirgaby J., Chang N.T., Gallo R.C.,

RA Wong-Staal F.; Complete nucleotide sequence of the AIDS virus, HTLV-III.";

RL Nature 313:277-284 (1985).

[illegible]

OY	1	LISTING:RGRLVCTYSVOVN 20
DB	588	LIGTWCSCGKICITTAVPWN 607
RESULT 9		
ID	ENV_HV1S3	STANDARD: PRT: 852 AA.
AC	P19549:	
DT	01-FEB-1991 (Rel. 17, Created)	
DT	01-FEB-1991 (Rel. 17, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].	
CN	ENV.	
OS	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).	
OC	Retroviridae; Retrovirus; Retroviralidae; Lentivirinae.	
OX	NCBI_TaxID=11690;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=90317906; PubMed=2370688;	
RA	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;	
RT	"Human immunodeficiency virus type 1 cellular host range,	
RT	replication, and cytopathicity are linked to the envelope region of	
RL	J. Virol. 64:4016-4020(1990).	
CC	-----	
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CC	entities requires a license agreement (See http://www.ebi.ac.uk/announcement/	
CC	or send an email to license@ebi.ac.uk).	
CC	-----	
DR	EMBL; M38427; AAA45067.1; -.	
DR	HIV; M38427; ENVSSRF33.	
DR	InterPro; IPR000328; Env GP41.	
DR	InterPro; IPR000777; GP120.	
DR	Pfam; PF00515; GP120_1.	
KW	Pfam; PF00517; GP41_1.	
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;	
KW	Signal.	
FT	SIGNAL	31 BY SIMILARITY.
FT	CHAIN	32 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507 TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53 BY SIMILARITY.
FT	DISULFID	118 BY SIMILARITY.
FT	DISULFID	125 BY SIMILARITY.
FT	DISULFID	130 BY SIMILARITY.
FT	DISULFID	156 BY SIMILARITY.
FT	DISULFID	219 BY SIMILARITY.
FT	DISULFID	229 BY SIMILARITY.
FT	DISULFID	297 BY SIMILARITY.
FT	DISULFID	331 BY SIMILARITY.
FT	DISULFID	377 BY SIMILARITY.
FT	DISULFID	412 BY SIMILARITY.
FT	CARBOHYD	87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	155 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	355 N-LINKED (GLCNAC. .) (POTENTIAL).

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FT CARBOHYD 385 385 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 852 AA; 96663 MW; EE7BFB8D23C9910D CRC64;

Query Match 65.4%; Score 83; DB 1; Length 852;
Best Local Similarity 60.0%; Pred. No. 3,7e-05;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

1 LLSLWCGRGLVCTSYQVN 20
588 LLGIWCGSKRLICTTAVPMN 607

RESULT 10
ENV_HV1MF STANDARD; PRT; 853 AA.
ID ENV_HV1MF
AC P19551;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11704;
RN [1]
RP MEDLINE=50317877; PubMed=1695254;
RX Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
RA Mashek A.;
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis."
RL J. Virol. 64:3792-3803(1990).
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CC -----
CC EMBL; M33943; AAA44850.1; -
DR HIV; M33943; ENVSMFA.
DR InterPro; IPR000328; ENV GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW signal.
FT SIGNAL 1 30
FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 510 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 203 BY SIMILARITY.
FT DISULFID 126 194 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 151 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 329 BY SIMILARITY.
FT DISULFID 376 443 BY SIMILARITY.
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FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6722ABA CRC64;

Query Match 65.4%; Score 83; DB 1; Length 853;
Best Local Similarity 60.0%; Pred. No. 3,7e-05;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

1 LLSLWCGRGLVCTSYQVN 20
590 LLGIWCGSKRLICTTAVPMN 609

RESULT 11
ENV_HV1A2 STANDARD; PRT; 855 AA.
ID ENV_HV1A2
AC P03378;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP MEDLINE=85090453; PubMed=25768227;
RX Sanchez-Pescador R., Power M.D., Barr P.J., Steiner K.S.,
RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2)."
RL Science 227:484-492(1985).
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CC -----
CC EMBL; X02007; AAB59882.1; -
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DR PIR: A03976; VCLJAZ2.
DR HIV: K02007; ENVSSSF2.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 208
FT DISULFID 125 199
FT DISULFID 130 155
FT DISULFID 221 250
FT DISULFID 231 242
FT DISULFID 299 333
FT DISULFID 380 442
FT DISULFID 387 415
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 200 200
FT CARBOHYD 233 233
FT CARBOHYD 244 244
FT CARBOHYD 265 265
FT CARBOHYD 279 279
FT CARBOHYD 292 292
FT CARBOHYD 298 298
FT CARBOHYD 304 304
FT CARBOHYD 334 334
FT CARBOHYD 341 341
FT CARBOHYD 358 358
FT CARBOHYD 364 364
FT CARBOHYD 388 388
FT CARBOHYD 394 394
FT CARBOHYD 400 400
FT CARBOHYD 408 408
FT CARBOHYD 445 445
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FT CARBOHYD 461 461
FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
FT CARBOHYD 855 AA; 97438 MW; A3BC20573AAC4142 CRC64;
SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC4142 CRC64;

Query Match 65.4%; Score 83; DB 1; Length 855;
Best Local Similarity 60.0%; Pred. No. 3.8e-05;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 LLSLWGRGRVCTSVQWN 20
DB 591 LLSLWGRGRVCTSVQWN 610

RESULT 12
ENV_HV10Y STANDARD; PRT; 855 AA.
AC P20888;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).

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OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11699;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148544; Pubmed=2559749;
RA Huet T., Daza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
individual presenting an atypical western blot.";
RL AIDS 3:707-715(1989).
CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
HEALTHY GABONESE INDIVIDUAL.
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CC -----
DR EMBL: M26727; AA0397.1; -.
DR HIV: M26727; ENV50Y1.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 335
FT DISULFID 381 442
FT DISULFID 388 415
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 142 142
FT CARBOHYD 145 145
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 192 192
FT CARBOHYD 202 202
FT CARBOHYD 239 239
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
FT CARBOHYD 294 294
FT CARBOHYD 300 300
FT CARBOHYD 306 306
FT CARBOHYD 336 336
FT CARBOHYD 359 359
FT CARBOHYD 389 389
FT CARBOHYD 395 395
FT CARBOHYD 399 399
FT CARBOHYD 405 405
FT CARBOHYD 458 458
FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
FT CARBOHYD 855 AA; 97476 MW; 9CF82A607ADB62DA CRC64;
SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADB62DA CRC64;

Query Match 65.4%; Score 83; DB 1; Length 855;
Best Local Similarity 60.0%; Pred. No. 3.8e-05;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Query Match 65.4%; Score 83; DB 1; Length 856;
 Best Local Similarity 60.0%; Pred. No. 3.8e-05;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLSLWGCGRRLVCYTSVQWN 20
 ||:||||:|:|:|
 Db 592 LLSLWGCGRRLVCYTSVQWN 611

Search completed: May 29, 2003, 10:36:58
 Job time : 6.4127 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:32:35 ; Search time 22.6984 Seconds
(without alignments)
199.707 Million cell updates/sec

Title: US-09-147-362A-2
Perfect score: 127
Sequence: 1 LLSLMGCRGLVCTSVQNMNET 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mmc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_prodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriopl.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	93.7	209	15	Q9IE66 human immun
2	116	91.3	116	15	O40458 human immun
3	116	91.3	124	15	O9IH07 human immun
4	116	91.3	126	15	O9IHV1 human immun
5	116	91.3	230	15	O9IEB2 human immun
6	116	91.3	240	15	O9IEB2 human immun
7	116	91.3	536	15	O9IEB5 human immun
8	116	91.3	879	15	O9WU9 human immun
9	116	91.3	880	15	O8Q7H1 human immun
10	116	91.3	900	15	O9QNZ8 human immun
11	115	90.6	104	15	O76163 human immun
12	115	90.6	216	15	O9IEC7 human immun
13	115	89.8	535	15	O9IEF2 human immun
14	114	89.8	125	15	O9IHU8 human immun
15	114	89.8	230	15	O9IEA9 human immun
16	114	89.8	238	15	O9DIK1 human immun

17	114	89.8	529	15	Q9IEE2 human immun
18	113	89.0	114	15	O40448 human immun
19	113	89.0	116	15	O40459 human immun
20	113	89.0	137	15	O9IHV5 human immun
21	113	89.0	172	15	O9IEB3 human immun
22	113	89.0	177	15	O9IEB0 human immun
23	113	89.0	208	15	O9IEA3 human immun
24	113	89.0	227	15	O9IE99 human immun
25	113	89.0	234	15	O9IEC2 human immun
26	113	89.0	342	15	O11942 human immun
27	113	89.0	418	15	O36547 human immun
28	113	89.0	502	15	O9IEE3 human immun
29	113	89.0	871	15	O57074 human immun
30	113	89.0	871	15	O8Q7H2 human immun
31	113	89.0	876	15	O8Q7H3 human immun
32	112	88.2	114	15	O40456 human immun
33	112	88.2	114	15	O40472 human immun
34	112	88.2	118	15	O40451 human immun
35	112	88.2	213	15	O9IEC4 human immun
36	112	88.2	225	15	O9IEA0 human immun
37	112	88.2	234	15	O9IEA6 human immun
38	112	88.2	532	15	O9IEF0 human immun
39	112	88.2	545	15	O9IED7 human immun
40	112	88.2	551	15	O9IEB1 human immun
41	112	88.2	863	15	O77377 human immun
42	112	88.2	872	15	O900Y5 human immun
43	111	87.4	116	15	O11941 human immun
44	111	87.4	116	15	O40449 human immun
45	111	87.4	118	15	O40450 human immun

ALIGNMENTS

RESULT 1
Q9IE66 PRELIMINARY; PRT; 209 AA.
ID Q9IE66
AC Q9IE66;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env polypeptide, gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCP107;
RA Roques P., Robertson D., Darnold F., Souquiere S., Mauciere P.,
RA Deleigne C., Brun-Vezinet F., Dormont D., Simon F.O.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AJ238862; CAB96300.1;
DR InterPro; IPR00328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 24116 MW; 91AC9BE2BF74B83 CRC64;

Query Match 93.7%; Score 119; DB 15; Length 209;
Best Local Similarity 86.4%; Pred.No. 1.7e-10;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSVQNMNET 22
Db |||||:||||:||||:||||:
56 LLSLMGCRGLVCTSVQNMNET.77

RESULT 2
O40458 PRELIMINARY; PRT; 116 AA.

AC 040458;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope transmembrane glycoprotein (Fragment).
OC Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=GROUP O;
RA Bibollet-Ruche F., Ekaza E., Peeters M., Delaporte E.;
RT "Molecular characterization of envelope transmembrane glycoprotein of
RT 14 new human immunodeficiency virus type 1 group O strains from
RT different African countries."
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y09774; CAA70913.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 116 AA; 13865 MW; 540F5B3B7AD849D8 CRC64;
Query Match 91.3%; Score 116; DB 15; Length 116;
Best Local Similarity 81.8%; Pred. No. 2.7e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LISTMCGRGLVCTSVQNMET 22
Db 39 LNLTMGCKGRILICYTSVQNMKT 60
RESULT 3
Q91HU7 PRELIMINARY; PRT; 124 AA.
AC Q91HU7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=97CM766;
RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O."
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229237; AAF71914.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 124 AA; 15287 MW; 105D515F114450F8 CRC64;
Query Match 91.3%; Score 116; DB 15; Length 124;
Best Local Similarity 81.8%; Pred. No. 2.9e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
Q91HV1

ID Q91HV1 PRELIMINARY; PRT; 126 AA.
AC Q91HV1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=97S203;
RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O."
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229233; AAF71910.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 126 AA; 15169 MW; 13FB101ECDF0DD CRC64;
Query Match 91.3%; Score 116; DB 15; Length 126;
Best Local Similarity 86.4%; Pred. No. 3e-10;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LISTMCGRGLVCTSVQNMET 22
Db 40 LNLTMGCKGRILICYTSVKMNS 61
RESULT 5
Q91EB2 PRELIMINARY; PRT; 230 AA.
AC Q91EB2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=YBP15.
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ236408; CAB96256.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 230 AA; 26705 MW; C1F744F82F51302D CRC64;

Query Match 91.3%; Score 116; DB 15; Length 230;
Best Local Similarity 81.8%; Pred. No. 5.3e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

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Q91E32 091E32 PRELIMINARY; PRT; 240 AA.
AC Q91E32;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE TM, GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCP11;
RA Roques P., Robertson D., Souquiere S., Diamond F., Mauciere P.,
  Depienne C., Brun-Vezinet F., Dormont D., Simon P.O.;
RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates.";
  Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AJ243365; CAB96335.1;
DR InterPro; IPR000328; Env_GP41.
PF pfam; PF00517; GP41; 1.
RN Transmembrane.
FT NON_TER 1 3
SQ SEQUENCE 240 AA; 27723 MW; 1E206E8D491A4197 CRC64;

Query Match 91.3%; Score 116; DB 15; Length 240;
Best Local Similarity 81.8%; Pred. No. 5.5e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLSLMGCRGLVCTSVQNMET 22
Db 60 LLSLMGCRGLVCTSVQNMET 81

RESULT 7
Q91E35 091E35 PRELIMINARY; PRT; 536 AA.
AC Q91E35;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VBF15;
RA Roques P., Robertson D., Diamond F., Souquiere S., Mauciere P.,
  Depienne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-GP41 region.";
  Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AJ133062; CAB96223.1;
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
PF pfam; PF00516; GP120; 1.
DR pfam; PF00517; GP41; 1.
RN AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 536 AA; 60419 MW; 0F533ABA08F552 CRC64;

Query Match 91.3%; Score 116; DB 15; Length 536;
Best Local Similarity 81.8%; Pred. No. 1.2e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLSLMGCRGLVCTSVQNMET 22
Db 361 LLSLMGCRGLVCTSVQNMET 382

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RESULT 8
Q9W1U9 09W1U9 PRELIMINARY; PRT; 879 AA.
AC Q9W1U9;
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Gp160 precursor.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VI686;
RX MEDLINE=99223950; PubMed=10207543;
RA Janssens W., Heyndrickx L., Van der Auwera G., Nkengasong J.,
  Baetens M., Vereecken K., Coppens S., Willems B., Franssen K.,
  Peeters M., Ndumbe P., Delaporte E., Van der Groen G.,
  "Outpatient genetic variability of HIV-1 group O.";
  AIDS 13:41-48(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VI686;
RX MEDLINE=96426454; PubMed=8828748;
RA Delaporte E., Janssens W., Peeters M., Buve A., Dibanga G.,
  Parret J.L., Ditsambou V., Georges Courbot M.C., Georges A.,
  Bourgeois A., Samb B., Henzel D., Heyndrickx L., Franssen K.,
  Van der Groen G., Larouz B., Mbe J.R.;
RT "Epidemiological and Molecular characteristics of HIV infection in
  Gabon (1986-1994).";
  AIDS 10:903-910(1996).
RL AIDS 10:903-910(1996).
DR EMBL; X96526; CAA65373.1;
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
PF pfam; PF00516; GP120; 1.
DR pfam; PF00517; GP41; 1.
RN AIDS; Coat protein; Glycoprotein; Polypeptide; Signal; Transmembrane.
FT SIGNAL 1 29
FT CHAIN 30 524
FT CHAIN 132 156
FT CHAIN 164 200
FT CHAIN 302 335
FT CHAIN 395 427
FT CHAIN 458 475
FT CHAIN 525 879
SQ SEQUENCE 879 AA; 99099 MW; BC6422ADDFA1A3409 CRC64;

Query Match 91.3%; Score 116; DB 15; Length 879;
Best Local Similarity 81.8%; Pred. No. 1.9e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLSLMGCRGLVCTSVQNMET 22
Db 605 LLSLMGCRGLVCTSVQNMET 626

RESULT 9
Q8Q7H1 08Q7H1 PRELIMINARY; PRT; 880 AA.
AC Q8Q7H1;
DT 01-JUN-2002 (TRENBLREL. 21, Created)
DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CMA407;
RX MEDLINE=21849375; PubMed=11860674;

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RA Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kapteue L.,
 RA Nganop C., Zekeng L., Gurtler L.G., Devare S.G., Brennan C.A.,
 RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
 RT Phylogenetic Clusters."
 RL AIDS Res. Hum. Retroviruses 18:269-283(2002).
 DR EMBL: AF83250; AAL9872.1; -
 SO SEQUENCE 880 AA; 99784 MW; F50D9358BED301EE CRC64;

Query Match 91.3%; Score 116; DB 15; Length 880;
 Best Local Similarity 81.8%; Pred. No. 1.9e-09;
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 1 LLSLMGCRGLVCTSYVQNMET 22
 ||:|||||:|||||:|||||:
 Db 608 LLSLMGCRGLVCTSYVQNMET 629

RESULT 10
 090N28 PRELIMINARY; PRT; 900 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENV protein.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=97CA-MP64SW/O;
 RX MEDLINE=99370180; PubMed=10438826;
 RA Peeters M., Liegeois F., Torimino N., Bourgeois A., Mpoudi E.,
 RA Verne L., Saman E., Delaporte E., Saragosti S.,
 RT "Characterization of a highly replicative intersubgroup M/O human
 RT immunodeficiency virus type 1 recombinant isolated from a Cameroonian
 RT patient."
 RL J. Virol. 73:7368-7375(1999).
 DR EMBL: AJ239083; CAB5242.1; -
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00517; GP41; 1.
 DR Pfam: PF00517; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SO SEQUENCE 900 AA; 100967 MW; FDB5E726A2537966 CRC64;

Query Match 91.3%; Score 116; DB 15; Length 900;
 Best Local Similarity 86.4%; Pred. No. 2e-09;
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LLSLMGCRGLVCTSYVQNMET 22
 ||:|||||:|||||:|||||:
 Db 628 LLSLMGCRGLVCTSYVQNMET 649

RESULT 11

ID 076163 PRELIMINARY; PRT; 104 AA.
 AC 076163.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GP41 ENV (Fragment).
 GN HIV-0 ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIV10DUR;
 RA Cohen J.H.M., Guetard D., Philbert F., Chamaret S., Tabary T.,
 RA Montagnier L., De Saint Martin J.;

RT "A novel HIV-1 O strain illustrates the diversity of the O group."
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X84328; CA959066.1; -
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 104
 SO SEQUENCE 104 AA; 12339 MW; D549218DD361067 CRC64;

Query Match 90.6%; Score 115; DB 15; Length 104;
 Best Local Similarity 81.8%; Pred. No. 3.5e-10;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 1 LLSLMGCRGLVCTSYVQNMET 22
 ||:|||||:|||||:|||||:
 Db 45 LLSLMGCRGLVCTSYVQNMET 66

RESULT 12

ID 091EC7 PRELIMINARY; PRT; 216 AA.
 AC 091EC7.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GP41 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCF03;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ236392; CAB96241.1; -
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 216
 SO SEQUENCE 216 AA; 25015 MW; 780C5F39CA6997C2 CRC64;

Query Match 90.6%; Score 115; DB 15; Length 216;
 Best Local Similarity 86.4%; Pred. No. 7.1e-10;
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LLSLMGCRGLVCTSYVQNMET 22
 ||:|||||:|||||:|||||:
 Db 55 LLSLMGCRGLVCTSYVQNMET 76

RESULT 13

ID 091EP2 PRELIMINARY; PRT; 535 AA.
 AC 091EP2.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Env polypeptide (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCF03;
 RA Roques P., Robertson D., Diamond F., Sousquiere S., Mauciere P.,
 RA Deplaine C., Brun-Vezinet F., Dormont D.,
 RT "HIV-1 group O phylogenetic analysis of C2-gp41 region.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ133055; CAB96216.1; -
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 535
 SQ SEQUENCE 535 AA; 59682 MW; 7234BE8378DD12C5 CRC64;

Query Match 90.6%; Score 115; DB 15; Length 535;
 Best Local Similarity 86.4%; Pred. No. 1.7e-09;
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSLMGCKGRLVCTSVQNMET 22
 DB 374 LLSLMGCKGRLVCTSVQNMET 395

LT 14

U8
 ID O9IHU8 PRELIMINARY; PRT; 125 AA.
 AC O9IHU8.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN GP41.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97CM756;
 RX MEDLINE=20386754; PubMed=10933623;
 RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,
 RA Plenzazek D., Schable C., Lai R.B.;
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV
 RT type 1 group O.";
 RL AIDS Res. Hum. Retroviruses 16:1075-1081 (2000).
 DR EMBL; AF229236; AAF71913.1; -
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW transmembrane.
 FT NON_TER 1
 FT NON_TER 125
 SQ SEQUENCE 125 AA; 15108 MW; EA2896C4B25FP342 CRC64;

ery Match 89.8%; Score 114; DB 15; Length 125;
 Best Local Similarity 77.3%; Pred. No. 6e-10;
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSLMGCKGRLVCTSVQNMET 22
 DB 37 LLSLMGCKGRLVCTSVQNMET 58

RESULT 15

O9IEA9 PRELIMINARY; PRT; 230 AA.
 ID O9IEA9
 AC O9IEA9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GP41 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YBF18;

RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ136411; CAB96259.1; -
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 230
 SQ SEQUENCE 230 AA; 26296 MW; 4B859829A69CC743 CRC64;

Query Match 89.8%; Score 114; DB 15; Length 230;
 Best Local Similarity 81.8%; Pred. No. 1.1e-09;
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSLMGCKGRLVCTSVQNMET 22
 DB 58 LLSLMGCKGRLVCTSVQNMET 79

Search completed: May 29, 2003, 10:39:15
 Job time : 23.6984 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20 ; Search time 29.333 Seconds
(without alignments)
99.938 Million cell updates/sec

Title: US-09-147-362A-3
Sequence: 1 LLSWGCKGRLVCTSVQNMET 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.GeneSeq 101002:*

- 1: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:*
- 7: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:*
- 8: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT:*
- 9: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:*
- 10: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:*
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- 19: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	100.0	22	19	AAW80461
2	124	97.6	22	19	AAW80466
3	122	96.1	22	19	AAW80462
4	120	94.5	40	17	AAW07346
5	118	92.9	22	19	AAW80460
6	118	92.9	22	19	AAW80463
7	117	92.1	32	19	AAW80469
8	113	89.0	22	19	AAW80464
9	113	89.0	22	19	AAW80465
10	113	89.0	40	17	AAW07352

11	113	89.0	113	20	AAV05565
12	113	89.0	200	21	AAV77373
13	113	89.0	215	20	AAV09499
14	113	89.0	215	20	AAV06983
15	113	89.0	215	21	AAV77374
16	113	89.0	245	20	AAV09492
17	113	89.0	245	20	AAV06977
18	113	89.0	245	21	AAV77369
19	113	89.0	281	20	AAV09507
20	113	89.0	373	20	AAV06979
21	113	89.0	373	20	AAV09500
22	113	89.0	460	20	AAV06984
23	113	89.0	460	21	AAV77375
24	113	89.0	474	21	AAV77371
25	113	89.0	474	20	AAV09504
26	113	89.0	488	20	AAV09504
27	113	89.0	490	20	AAV09494
28	113	89.0	490	20	AAV06978
29	113	89.0	490	21	AAV77370
30	113	89.0	526	20	AAV09505
31	113	89.0	618	20	AAV09496
32	113	89.0	618	20	AAV06980
33	113	89.0	618	21	AAV77372
34	113	89.0	706	20	AAV09503
35	113	89.0	715	20	AAV05525
36	113	89.0	736	20	AAV09502
37	113	89.0	873	20	AAV09501
38	113	89.0	873	21	AAV06985
39	113	89.0	873	21	AAV77376
40	111	87.4	32	19	AAW80470
41	111	87.4	32	19	AAW12212
42	111	86.6	22	19	AAW80459
43	110	86.6	32	19	AAW80471
44	110	86.6	33	21	AAW12231
45	110	86.6	40	17	AAW07343

ALIGNMENTS

RESULT 1
AAW80461
ID AAW80461 standard; peptide: 22 AA.
AC AAW80461;
XX 28-JAN-1999 (first entry)
DT Peptide derived from a conserved sequence of group O human HIV.
XX Group O human immune deficiency virus; HIV; detection: infection.
DE Synthetic.
XX Immune deficiency virus.
OS W09845323-A1.
XX 15-OCT-1998.
PD 06-APR-1998; 98WO-FR00691.
XX 24-FEB-1998; 98FR-0002212.
PR 09-APR-1997; 97FR-0004356.
XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
XX Chebreaux DMB, Delagneau JFH, Gadelje SJX, Rieunier FY;
XX WPI, 1998-583190/49.
PT New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

XX
CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 100.0%; Score 127; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 6.2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCTSVQNNET 22
DB 1 LLSWGCKGRIVCTSVQNNET 22

LT 2
AAW80466

ID AAW80466 standard; peptide; 22 AA.

AC AAW80466;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

PN MO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOPI DIAGNOSTICS SA.

PI Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

PI 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
PT human immune deficiency virus of group O

PS Claim 6; Page 43; 55pp; French.

XX AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 97.6%; Score 124; DB 19; Length 22;

Best Local Similarity 95.5%; Pred. No. 1.5e-09;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCTSVQNNET 22
DB 1 LLSWGCKGRIVCTSVQNNET 22

RESULT 3

AAW80462

ID AAW80462 standard; peptide; 22 AA.

AC AAW80462;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

PN MO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOPI DIAGNOSTICS SA.

PI Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

PI 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
PT human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

XX AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 96.1%; Score 122; DB 19; Length 22;

Best Local Similarity 95.5%; Pred. No. 2.8e-09;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCTSVQNNET 22
DB 1 LLSWGCKGRIVCTSVQNNET 22

RESULT 4

AAW07346

ID AAW07346 standard; peptide; 40 AA.

AC AAW07346;

DT 03-JUN-1997 (first entry)

DE Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).

KM Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;
KM C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
KM primer; hybridisation; amplification; PCR; polymerase chain reaction;
KM immunogen; antibody.

OS Human immunodeficiency virus type 1.

PN MO9627013-A1.

PD 06-SEP-1996.

XX 26-FEB-1996; 96WO-FR00294.
 XX 27-FEB-1995; 95FR-0002236.
 XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX Chaiix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F,
 XX WPI; 1996-412779/41.
 XX N-PSDB; AAT44922.
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 XX antibodies - useful for diagnosis, screening and typing, or as
 XX immunogens
 XX Claim 12; Page 34; 71pp; French.
 XX Human immunodeficiency virus type 1 (HIV-1) strains are currently
 XX divided into 2 major groups based on the nucleotide sequences of the
 XX envelope gene (env): group M containing sub-groups A-G, and group O
 XX containing the strains AN70 and WPS180. The invention relates to the
 XX discovery of several new strains of HIV-1 which can be placed in group O,
 XX based on the partial sequences of the C23-env, gp41 and gag genes (see
 XX AAT44907-39 and AAM07329-64). The novel strains have been deposited as
 XX retroviruses CNCM I-1544 (BCF02 (BSS)), 1543 (BCF01 (FAN)), 1546 (BCF07
 XX (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
 XX presented here is from the strain BCF07 (MAN) and corresponds to a
 XX fragment of the gp41 protein encoded by the env gene. The nucleic acids
 XX can be used to detect gp. O HIV-1 strains by hybridisation or (as
 XX primers) by gene amplification, also for screening and typing of such
 XX strains. Peptides encoded by the nucleic acids can be used as immunogens
 XX to raise Ab for detecting gp. O HIV-1.
 XX Sequence 40 AA:
 SQ Query Match 94.5%; Score 120; DB 17; Length 40;
 Best Local Similarity 90.9%; Pred. No. 8.9e-09;
 Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLSWGCKGRIVCYTSVQNNET 22
 DB 19 LLSWGCKGRIVCYTSVQNNET 40
 RESULT 5
 AAM80460 standard; peptide; 22 AA.
 AC AAM80460;
 XX 28-JAN-1999 (first entry)
 XX Peptide derived from a conserved sequence of group O human HIV.
 XX Group O human immune deficiency virus; HIV; detection; infection.
 XX Synthetic.
 XX Immune deficiency virus.
 OS WO9845323-A1.
 XX 15-OCT-1998.
 PD 06-APR-1998; 98WO-FR00691.
 XX 24-FEB-1998; 98FR-0002212.
 XX 09-APR-1997; 97FR-0004356.
 XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 XX Chenebaux DMB, Delagneau JFH, Gabelle SUX, Rieunier FY;

XX WPI; 1998-583190/49.
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 XX human immune deficiency virus of group O
 XX Claim 6; Page 42; 55pp; French.
 XX AAM80459-74 represent synthetic peptides (either linear or cyclised by
 XX Cys-Cys disulphide bonds). The peptides represent variable sequences
 XX connected around short highly conserved sequences present in isolates
 XX of group O human immune deficiency virus (HIV). The peptides are
 XX useful as immunological reagents for detecting infection by group O
 XX human immune deficiency virus (HIV).
 XX Sequence 22 AA;
 SQ Query Match 92.9%; Score 118; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 9.3e-09;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LLSWGCKGRIVCYTSVQNNET 22
 DB 1 LLSWGCKGRIVCYTSVQNNET 22
 RESULT 6
 AAM80463 standard; peptide; 22 AA.
 AC AAM80463;
 XX 28-JAN-1999 (first entry)
 XX Peptide derived from a conserved sequence of group O human HIV.
 XX Group O human immune deficiency virus; HIV; detection; infection.
 XX Synthetic.
 XX Immune deficiency virus.
 OS WO9845323-A1.
 XX 15-OCT-1998.
 PD 06-APR-1998; 98WO-FR00691.
 XX 24-FEB-1998; 98FR-0002212.
 XX 09-APR-1997; 97FR-0004356.
 XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 XX Chenebaux DMB, Delagneau JFH, Gabelle SUX, Rieunier FY;
 XX WPI; 1998-583190/49.
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 XX human immune deficiency virus of group O
 XX Claim 6; Page 42; 55pp; French.
 XX AAM80459-74 represent synthetic peptides (either linear or cyclised by
 XX Cys-Cys disulphide bonds). The peptides represent variable sequences
 XX connected around short highly conserved sequences present in isolates
 XX of group O human immune deficiency virus (HIV). The peptides are
 XX useful as immunological reagents for detecting infection by group O
 XX human immune deficiency virus (HIV).
 XX Sequence 22 AA;
 SQ Query Match 92.9%; Score 118; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 9.3e-09;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLYCTSVQNMNET 22
 DB 1 LLSWGCKGRLYCTSVQNMNET 22

RESULT 7

AAW80469
 ID AAW80469 standard; peptide; 32 AA.

AC AAW80469;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KW Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

PS Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PS 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOPI DIAGNOSTICS SA.

PI Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

DR WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

PS Claim 6; Page 44; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

XX Sequence 32 AA;

Query Match 92.1%; Score 117; DB 19; Length 32;

Best Local Similarity 86.4%; Pred. No. 1.8e-08;

Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLYCTSVQNMNET 22
 DB 1 LLSWGCKGRLYCTSVQNMNET 32

RESULT 8

AAW80464
 ID AAW80464 standard; peptide; 22 AA.

AC AAW80464;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KW Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

PS Immune deficiency virus.

XX WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PS 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOPI DIAGNOSTICS SA.

PI Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

DR WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

PS Claim 6; Page 43; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 89.0%; Score 113; DB 19; Length 22;

Best Local Similarity 81.8%; Pred. No. 4.1e-08;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLYCTSVQNMNET 22
 DB 1 LLSWGCKGRLYCTSVQNMNET 22

AAW80465
 ID AAW80465 standard; peptide; 22 AA.

AC AAW80465;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KW Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

PS Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PS 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOPI DIAGNOSTICS SA.

PI Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

DR WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

PS Claim 6; Page 43; 55pp; French.

XX
CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).
XX
SQ Sequence 22 AA;
Query Match 89.0%; Score 113; DB 19; Length 22;
Best Local Similarity 86.4%; Pred. No. 4.1e-08;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 LLSMGCKGRVLCYTSVQNMET 22
1 LLSMGCKGRVLCYTSVQNMET 22
Db 1 LLSMGCKGRVLCYTSVQNMET 22

XX
XX AAW07352 standard; peptide: 40 AA.
XX
XX AAW07352;
XX
XX 03-JUN-1997 (first entry)
XX
XX Partial sequence of gp41 from HIV-1 gp. O strain BCF13.
XX
XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
XX C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
XX primer; hybridisation; amplification; PCR; polymerase chain reaction;
XX immunogen; antibody.
XX
XX Human immunodeficiency virus type 1.
XX
XX W09627013-A1.
XX
XX 06-SEP-1996.
XX
XX 26-FEB-1996; 96WO-FR00294.
XX
XX 27-FEB-1995; 95FR-0002235.
XX
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Chaiix-Baudier ML, Lousseert-Ajaka I, Ly T, Saragosti S, Simon F;
XX WPI; 1996-412779/41.
XX
XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
XX antibodies - useful for diagnosis, screening and typing, or as
XX immunogens
XX
XX Claim 12; Page 46; 71pp; French.
XX
XX Human immunodeficiency virus type 1 (HIV-1) strains are currently
XX divided into 2 major groups based on the nucleotide sequences of the
XX envelope gene (env): group M containing sub-groups A-G, and group O
XX containing the strains ANR70 and WPS180. The invention relates to the
XX discovery of several new strains of HIV-1 which can be placed in group O,
XX based on the partial sequences of the C2V3-env, gp41 and gag genes (see
XX AAT4907-39 and AAW07329-64). The novel strains have been deposited as
XX retroviruses CCMC I-1544 (BCF02 (RSS)), 1543 (BCF01 (PAN)), 1546 (BCF07
XX (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
XX presented here is from the strain BCF13 and corresponds to a fragment of
XX the gp41 protein encoded by the env gene. The nucleic acids can be used
XX to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene
XX amplification, also for screening and typing of such strains. Peptides
XX encoded by the nucleic acids can be used as immunogens to raise Ab for
XX detecting gp. O HIV-1.

SQ Sequence 40 AA;
Query Match 89.0%; Score 113; DB 17; Length 40;
Best Local Similarity 86.4%; Pred. No. 7.3e-08;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 LLSMGCKGRVLCYTSVQNMET 22
1 LLSMGCKGRVLCYTSVQNMET 22
Db 19 LLSMGCKGRVLCYTSVQNMET 40

XX
XX AAW05565 standard; Protein; 113 AA.
XX
XX AAW05565;
XX
XX 19-JUL-1999 (first entry)
XX
XX HIV-1 group O isolate MP539-PBMC gp41 antigen.
XX
XX HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
XX vaccine; diagnosis; AIDS.
XX
XX Human immunodeficiency virus type 1.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 65
XX /note= "encoded by AMW"
XX
XX Misc-difference 74
XX /note= "encoded by ATR"
XX
XX Misc-difference 84
XX /note= "encoded by GAK"
XX
XX Misc-difference 86
XX /note= "encoded by AGY"
XX
XX W09904011-A2.
XX
XX 28-JAN-1999.
XX
XX 20-JUL-1998; 98WO-EP04522.
XX
XX 18-JUL-1997; 97EP-0870110.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
XX WPI; 1999-132255/11.
XX
XX N-PSDB; AAY05565.
XX
XX New isolated HIV-1 group O strains - used to produce
XX polynucleotides, antigens and antibodies for use in diagnosis and in
XX vaccines for prevention of HIV-1 infection
XX
XX Claim 3; Fig 6; 162pp; English.
XX
XX The present sequence is an antigen of the gp41 protein of HIV-1
XX group O (Outlier) strain MP539-PBMC, a Cameroon isolate. The
XX invention relates to new HIV-1 group O antigens (see AAY05565-625),
XX and the use of these antigens, or nucleic acids encoding them (see
XX AAY25154-80), in the diagnosis and prophylaxis of AIDS. They can be
XX used as reagents for detecting HIV-1 group O infection and for
XX differentiating different types of HIV-1 group O infection.
XX Vaccines that provide protective immunity against HIV-1 infection, in
XX particular against HIV-1 group O infection, comprise at least one
XX HIV-1 type O antigen, a nucleic acid encoding such an antigen, a
XX virus-like particle comprising such an antigen, or an attenuated
XX form of an HIV-1 type O strain. The invention also relates to new
XX HIV-1 group O strains, mostly from patients from Cameroon and its
XX neighbouring countries.
XX
SQ Sequence 113 AA;

```

Query Match      89.0%; Score 113; DB 20; Length 113;
Best Local Similarity 81.8%; Pred. No. 1,9e-07;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 1
Oy      1  LLSWGCKGRVLCVTSVOMNET 22
      ||| ||||| ||||| |||
Db      39  LNLMGCKGRILCTTSVOMNKT 60

RESULT 12
AAV77373
ID  AAV77373 standard; Protein: 200 AA.
XX
XX  AAV77373;
AC
XX
XX  22-MAY-2000 (first entry)
DT
XX
XX  HIV-1 group O env gp120/gp41 pCO-5 recombinant protein, SEQ ID NO:56.
DE

HIV-1 group O env; gp120; gp41; glycoprotein; monoclonal antibody;
immunoreassay; positive control; affinity purification; therapeutic;
Escherichia coli; antigen; synthetic gene construction; muten;
deletion mutation.

Human immunodeficiency virus type 1 group O isolate HAM112.
Synthetic.
OS
XX
XX  MO200004363-A2.
XX
XX  27-JAN-2000.
PD
XX
XX  09-JUL-1999; 99MO-US15469.
PF
XX
XX  14-JUL-1998; 98US-0115171.
PR
XX
XX  (ABBO ) ABBOTT LAB.
XX
XX
XX  Scheffel JW, Hackett JR, Tyner JD, Hickman RK,
PI
XX
XX  WPI: 2000-171290/15.
XX
XX  N-PSDB; AAZ90284.
DR
XX
XX
XX  Novel monoclonal antibodies useful as positive control reagent for
PT  detecting human immunodeficiency virus infections and diagnosing,
PT  evaluating or prognosing viral disease -
PT
XX
XX  Example 3; Fig 9; 14bp; English.

The invention relates to anti-HIV-1 group O monoclonal antibodies, which
may be used as positive control reagents in immunoassays to detect and
differentiate HIV-1 infections. The invention also encompasses a
monoclonal antibody which binds specifically to an HIV-1 group O
antigen, which has no more than 15% cross reactivity to a corresponding
antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a
method of using a monoclonal antibody as a positive control reagent in
an immunoassay for the detection of anti HIV-1 group O antibodies. The
monoclonal antibodies are useful as positive control reagents in
immunoassays capable of detecting anti-HIV-1 Group O antibodies. Such
immunoassays involve coupling a monoclonal antibody with HIV group-1
antigen and detecting the antigen-antibody complex. The monoclonal
antibodies of the invention would be used to ensure that the reagents
provided to detect HIV-1 group O antibody were performing properly. The
monoclonal antibodies may also can be immobilised on a matrix and used
for affinity purification of specific HIV-1 group O-derived proteins
from cell cultures or biological tissues. The monoclonal antibodies can
also be used for generating chimeric antibodies for therapeutic use.
Different synthetic, recombinant or purified antibodies which identify
CC different epitopes of HIV antigens can be used in combination in assay
CC diagnosis, evaluate, or prognosticate HIV disease condition. The
CC monoclonal antibodies are also useful for differentiating HIV-1 Group O
CC antigens from HIV-group M and HIV-2 antigens. Sequences AAV77369-V77375
CC represent recombinant HIV-1 group O env antigens encoded by the synthetic
CC

```

CC gene AAZ90280-Z90286. The recombinant HIV-1 env proteins contain
CC various deletions relative to the native HAM112 isolate env protein
CC (AAV7376). The recombinant HIV-1 group O antigens were purified and used
CC to screen hybridoma cultures.
XX

SQ Sequence 200 AA;

Query Match 89.0%; Score 113; DB 21; Length 200;
Best Local Similarity 81.8%; Pred. No. 3.3e-07;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0.

QY 1 LLSWGCKGRILVCYTSTVOVNRET 22
||:|||||:|||:||||
Db 112 LLNLWCGKRLICTYSVKMNET 133

RESULT 13
AAO9499
ID AAO9499 standard; Protein; 215 AA.
XX
AC AAY09499;
XX
DT 15-JUL-1999 (first entry)
XX
DE HIV-1 Group O env polypeptide pGO-8PL.
XX
KW HIV; human immunodeficiency virus; antigen; detection; antibody;
KW differentiation; Group O; env; immunogen; immunoassay.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9909179-A2.
XX
PD 25-FEB-1999.
PR 17-AUG-1998; 98MO-US17014.
PR 15-AUG-1997; 97US-0911824.
PA (ABBO) ABBOTT LAB.
PI Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J,
DR WPI, 1999-190167/16.
XX N-PsDB; AAX56078.
XX

New isolated HIV-1 Group O env polypeptides - used for the
PT detection of anti-HIV antibodies and for the production of
PT antibodies for use in detection, purification and therapy
XX
XX Claim 17; Fig 5; 13pp; English.

The present invention describes (A) an isolated HIV-1 Group O env
polypeptide. Also described are: (1) an isolated HIV-1 Group O env
polypeptide comprising an immunoreactive portion of a polypeptide as in
(A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);
(3) an antigen construct comprising a first HIV-1 Group O env polypeptide
fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
comprising a fusion of at least one HIV-1 Group O env polypeptide with at
least one HIV-1 Group M env polypeptide; (5) an antigen construct
comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env
polypeptide, and at least one additional HIV-1 polypeptide; (6) an
antigen construct comprising a first HIV-2 env polypeptide fused to a
second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as
in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a
host cell transformed by an expression vector as in (8); and (10) an
immunoassay kit for the detection of antibodies to HIV-1 comprising an
antigen construct as in (3)-(6). The antigen constructs can be used for
the detection of anti-HIV-1 antibodies in test samples. They can also be
used as immunogens to produce antibodies. The antibodies can be used to
purify HIV polypeptides, for therapy and for detection of HIV
polypeptides.

SO Sequence 215 AA;

Query Match 89.0%; Score 113; DB 20; Length 215;
 Best Local Similarity 81.8%; Pred. No. 3.5e-07;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LLSMGGCKRLVCTSVQNNET 22
 ||:|||||:|||||:
 127 LNLNMGCKRLVCTSVQNNET 148

RESULT 14
 ID AAY06983 standard; Protein; 215 AA.
 AC AAY06983;
 DT 06-JUL-1999 (first entry)
 XX Recombinant pCO-8PL protein.
 KM HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;
 OS antibody; assay.
 OS Synthetic.
 OS Human immunodeficiency virus type 1.
 FH Key Location/Qualifiers
 FT Protein 2..46
 FT Peptide /note="gp120 sequence"
 FT 47..245
 FT /note="gp41 sequence"

W09909410-A2.
 25-FEB-1999.
 07-AUG-1998; 98WO-US15506.
 15-AUG-1997; 97US-0912129.
 (ABBO) ABBOTT LAB.
 Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;
 Necklaws EC, Vallari AS, Varitek V;
 WPI; 1999-190224/16.
 N-PSDB; AAX37193.

New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
 can be used in field assay, requiring no electricity and less
 specialised equipment

Claim 1; Fig 5; 104pp; English.

The invention relates to a rapid assay for simultaneous detection and
 differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
 method comprises (a) contacting the sample with a strip containing at
 least one immobilised capture reagent per analyte and on which the
 sample moves from the proximal to the distal end by capillary action,
 under conditions sufficient to form capture reagent/analyte complexes,
 and (b) determining the presence of analyte(s) by detecting a visible
 colour change at the capture reagent site on the strip wherein the
 capture reagent for HIV-1 group O comprises a polypeptide shown in
 CC AAY06977-80 and AAY06983-84; and that for HIV-1 group M comprises a
 CC polypeptide shown in AAY06982; and that for HIV-2 comprises the
 CC polypeptide shown in AAY06981. The invention is used to screen patients
 CC for antibodies to HIV-1 types O and M, and HIV-2. The invention will be
 CC particularly useful in places and situation where equipment and/or
 CC electricity is not available. The invention provides a screening method
 CC which is faster and requires less equipment than prior art methods. The
 CC present sequence represents a amino acid sequence of the recombinant
 CC pCO-8PL protein which acts as a capture reagent for HIV-1 group O.

XX SQ Sequence 215 AA;

Query Match 89.0%; Score 113; DB 20; Length 215;
 Best Local Similarity 81.8%; Pred. No. 3.5e-07;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LLSMGGCKRLVCTSVQNNET 22
 ||:|||||:|||||:
 127 LNLNMGCKRLVCTSVQNNET 148

RESULT 15
 AAY77374
 ID AAY77374 standard; Protein; 215 AA.
 AC AAY77374;
 DT 22-MAY-2000 (first entry)
 XX HIV-1 group O env gp120/gp41 pCO-8PL recombinant protein, SEQ ID NO:58.
 DE HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;
 KM immunosassay; positive control; affinity purification; therapeutic;
 KM Escherichia coli; antigen; synthetic gene construction; mutain;
 KM deletion mutation.
 OS Human immunodeficiency virus type 1 group O isolate HAM112.
 OS Synthetic.
 OS W0200004383-A2.
 PD 27-JAN-2000.
 PF 09-JUL-1999; 99WO-US15469.
 PR 14-JUL-1998; 98US-0115171.
 (ABBO) ABBOTT LAB.
 Scheffell JM, Hackett JR, Tyner JD, Hickman RK;
 WPI; 2000-171290/15.
 N-PSDB; AAZ90285.

Novel monoclonal antibodies useful as positive control reagent for
 detecting human immunodeficiency virus infections and diagnosing,
 PT evaluating or prognosing viral disease -

Example 3; Fig 5; 148pp; English.

The invention relates to anti-HIV-1 group O monoclonal antibodies, which
 CC may be used as positive control reagents in immunoassays to detect and
 CC differentiate HIV-1 infections. The invention also encompasses a
 CC monoclonal antibody which binds specifically to an HIV-1 group O
 CC antigen, which has no more than 15% cross reactivity to a corresponding
 CC antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a
 CC method of using a monoclonal antibody as a positive control reagent in
 CC an immunoassay for the detection of anti HIV-1 group O antibodies. The
 CC monoclonal antibodies are useful as positive control reagents in
 CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such
 CC immunoassays involve coupling a monoclonal antibody with HIV group-1
 CC antigen and detecting the antigen-antibody complex. The monoclonal
 CC antibodies of the invention would be used to ensure that the reagent
 CC provided to detect HIV-1 group O antibody were performing properly. The
 CC monoclonal antibodies may also can be immobilised on a matrix and used
 CC for affinity purification of specific HIV-1 group O-derived proteins
 CC from cell cultures or biological tissues. The monoclonal antibodies can
 CC also be used for generating chimeric antibodies for therapeutic use.
 CC Different synthetic, recombinant or purified antibodies which identify
 CC different epitopes of HIV antigens can be used in combination in assay to
 CC diagnose, evaluate, or prognosticate HIV disease condition. The
 CC monoclonal antibodies are also useful for differentiating HIV-1 Group O

CC antigens from HIV-group M and HIV-2 antigens. Sequences AAY77369-Y77375
CC represent recombinant HIV-1 group O env antigens encoded by the synthetic
CC genes AA790280-290286. The recombinant HIV-1 env proteins contain
CC various deletions relative to the native HAM12 isolate env protein
CC (AAY77376). The recombinant HIV-1 group O antigens were purified and used
CC to screen hybridoma cultures.
XX

SQ Sequence 215 AA;

Query Match 89.0%; Score 113; DB 21; Length 215;
Best Local Similarity 81.8%; Pred. No. 3.5e-07;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSSMGCKGRIVCYTSVQNNET 22
||:|||||:|||||:
Db 127 LNLWGCCKGRILCYTSVQNNET 148

Search completed: May 29, 2003, 10:36:21
Time : 30.333 secs

Thu May 29 15:25:09 2003

US-09-147-362a-3.rai

Page 1

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:36 ; Search time 9.95238 Seconds
(Without alignments)
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Title: US-09-147-362a-3
Perfect score: 127
Sequence: 1 LLSMGCGRIVCYTSVQNNET 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfilltest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	120	94.5	40	3	US-08-894-699-39
2	120	94.5	40	4	US-09-444-410-39
3	113	89.0	40	3	US-08-894-699-68
4	113	89.0	40	4	US-09-444-410-68
5	113	89.0	215	2	US-08-912-129A-58
6	113	89.0	375	2	US-08-912-129A-48
7	113	89.0	373	2	US-08-912-129A-52
8	113	89.0	460	2	US-08-912-129A-60
9	113	89.0	490	2	US-08-912-129A-50
10	113	89.0	618	2	US-08-912-129A-54
11	113	89.0	873	2	US-08-912-129A-61
12	111	87.4	33	4	US-09-433-428D-6
13	111	86.6	33	4	US-09-433-428D-25
14	110	86.6	40	4	US-08-894-699-36
15	110	86.6	40	4	US-09-444-410-36
16	110	86.6	356	1	US-08-602-713-12
17	110	86.6	356	1	US-08-989-493-12
18	109	85.8	37	4	US-08-817-441-86
19	109	85.8	41	4	US-08-894-699-69
20	109	85.8	41	4	US-09-444-410-69
21	109	85.8	200	4	US-08-965-056-104
22	108	85.0	33	4	US-09-433-428D-30
23	108	85.0	41	3	US-08-894-699-67
24	108	85.0	41	4	US-09-444-410-67
25	107	84.3	33	4	US-09-433-428D-8
26	107	84.3	40	3	US-08-894-699-41
27	107	84.3	40	3	US-08-894-699-42

28	107	84.3	40	4	US-09-444-410-41	Sequence 41, Appl
29	107	84.3	40	4	US-09-444-410-42	Sequence 42, Appl
30	106	83.5	37	4	US-08-817-441-94	Sequence 94, Appl
31	106	83.5	40	3	US-08-894-699-37	Sequence 37, Appl
32	106	83.5	40	4	US-09-444-410-37	Sequence 37, Appl
33	106	83.5	104	4	US-08-817-441-100	Sequence 100, Appl
34	105	82.7	40	3	US-08-894-699-40	Sequence 40, Appl
35	105	82.7	40	4	US-09-444-410-40	Sequence 40, Appl
36	104	81.9	23	4	US-09-433-428D-68	Sequence 68, Appl
37	104	81.9	33	4	US-09-433-428D-1	Sequence 1, Appl
38	104	81.9	33	4	US-09-433-428D-4	Sequence 4, Appl
39	104	81.9	33	4	US-09-433-428D-7	Sequence 7, Appl
40	104	81.9	33	4	US-09-433-428D-15	Sequence 15, Appl
41	104	81.9	42	3	US-08-894-699-66	Sequence 66, Appl
42	104	81.9	42	4	US-09-444-410-66	Sequence 66, Appl
43	103	81.1	33	4	US-09-433-428D-5	Sequence 5, Appl
44	103	81.1	33	4	US-09-433-428D-14	Sequence 14, Appl
45	103	81.1	33	4	US-09-433-428D-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-894-699-39
Sequence 39, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSBERT-AJARA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBION, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

/ MOLECULE TYPE: peptide
US-08-894-699-39

Query Match 94.5%; Score 120; DB 3; Length 40;
Best Local Similarity 90.9%; Pred. No. 9.3e-11;
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCYTSVQNMET 22
||:|||||
DB 19 LLSWGCKGRLVCYTSVQNMET 40

RESULT 2
US-09-444-410-39

/ Sequence 39, Application US/09444410
/ Patent No. 6270975

/ GENERAL INFORMATION:

/ APPLICANT: SIMON, FRANCOIS

/ APPLICANT: SARAGOSTI, SENTOB

/ APPLICANT: LOUSSEST-AJAKA, IBITISSAM

/ APPLICANT: LY, THOAI-DUONG

/ APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

/ TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

/ NUMBER OF SEQUENCES: 81

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

/ STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

/ CITY: ARLINGTON

/ STATE: VA

/ COUNTRY: USA

/ ZIP: 22202

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/444,410

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 08/894,699

/ FILING DATE:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: FR 95/02236

/ FILING DATE: 27-FEB-1995

/ ATTORNEY/AGENT INFORMATION:

/ NAME: OBLON, NORMAN F.

/ REGISTRATION NUMBER: 24,614

/ REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 703-413-3000

/ TELEFAX: 703-413-2220

/ INFORMATION FOR SEQ ID NO: 39:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 40 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

US-09-444-410-39

RESULT 3
US-08-894-699-68

/ Sequence 68, Application US/08894699
/ Patent No. 6030769

/ GENERAL INFORMATION:

/ APPLICANT: SIMON, FRANCOIS

/ APPLICANT: SARAGOSTI, SENTOB

/ APPLICANT: LOUSSEST-AJAKA, IBITISSAM

/ APPLICANT: LY, THOAI-DUONG

/ APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

/ TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

/ NUMBER OF SEQUENCES: 81

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

/ STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

/ CITY: ARLINGTON

/ STATE: VA

/ COUNTRY: USA

/ ZIP: 22202

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/894,699

/ FILING DATE: 01-DEC-1997

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: PCT/FR96/00294

/ FILING DATE: 26-FEB-1996

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: FR 95/02236

/ FILING DATE: 27-FEB-1995

/ ATTORNEY/AGENT INFORMATION:

/ NAME: OBLON, NORMAN F.

/ REGISTRATION NUMBER: 24,614

/ REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 703-413-3000

/ TELEFAX: 703-413-2220

/ INFORMATION FOR SEQ ID NO: 68:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 40 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

US-08-894-699-68

Query Match 89.0%; Score 113; DB 3; Length 40;
Best Local Similarity 86.4%; Pred. No. 9.4e-10;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCYTSVQNMET 22
||:|||||
DB 19 LLSWGCKGRLVCYTSVQNMET 40

RESULT 4
US-09-444-410-68

/ Sequence 68, Application US/09444410
/ Patent No. 6270975

/ GENERAL INFORMATION:

/ APPLICANT: SIMON, FRANCOIS

/ APPLICANT: SARAGOSTI, SENTOB

/ APPLICANT: LOUSSEST-AJAKA, IBITISSAM

/ APPLICANT: LY, THOAI-DUONG

/ APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-68
Query Match 89.0%; Score 113; DB 4; Length 40;
Best Local Similarity 86.4%; Pred. No. 9.4e-10;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
1 LLSWGCKGRIVCYTSVQNMET 22
||:|||||||:||||
19 LLSWGCKGRIVCYTSVQNMET 40
RESULT 5
US-08-912-129A-58
Sequence 58, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANANDRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckerts, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-912-129A-58
Query Match 89.0%; Score 113; DB 2; Length 215;
Best Local Similarity 81.8%; Pred. No. 5.3e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
1 LLSWGCKGRIVCYTSVQNMET 22
||:|||||||:||||
Db 127 LLSWGCKGRIVCYTSVQNMET 146
RESULT 6
US-08-912-129A-48
Sequence 48, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANANDRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ. ID NO.: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-48

Query Match
Best Local Similarity 89.0%; Score 113; DB 2; Length 245;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db
1 LLSWGCKGRILVCTSVQNMET 22
||:|||||:|||||:|||||
127 LNLWGCKGRILVCTSVQNMET 148

RESULT 7
US-08-912-129A-52
Sequence 52, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITEK, VINCENT A. JR.
APPLICANT: NECKLAWS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-912-129A-52

Query Match
Best Local Similarity 89.0%; Score 113; DB 2; Length 373;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db
1 LLSWGCKGRILVCTSVQNMET 22
||:|||||:|||||:|||||
127 LNLWGCKGRILVCTSVQNMET 148

RESULT 8
US-08-912-129A-60
Sequence 60, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITEK, VINCENT A. JR.
APPLICANT: NECKLAWS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-60

Query Match
Best Local Similarity 89.0%; Score 113; DB 2; Length 460;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db
1 LLSWGCKGRILVCTSVQNMET 22
||:|||||:|||||:|||||
372 LNLWGCKGRILVCTSVQNMET 393

RESULT 9

US-08-912-129A-50
 ; Sequence 50, Application US/08912129A
 ; Patent No. 5922533
 ; GENERAL INFORMATION:
 ; APPLICANT: VALLARI, ANADRUZELA S.
 ; APPLICANT: HACKETT, JOHN JR.
 ; APPLICANT: HICKMAN, ROBERT K.
 ; APPLICANT: VARITEK, VINCENT A. JR.
 ; APPLICANT: NECKLAWS, ELIZABETH A.
 ; APPLICANT: GOLDEN, ALAN M.
 ; APPLICANT: BRENNAN, CATHERINE A.
 ; APPLICANT: DEVARE, SUSHIL G.
 ; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
 ; NUMBER OF SEQUENCES: 89
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 ; OPERATING SYSTEM: MS-DOS (Windows 95)
 ; SOFTWARE: Microsoft Word (ASCII format output)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/912,129A
 ; FILING DATE: 15-AUG-1997
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Danckers, Andreas M.
 ; REGISTRATION NUMBER: 32,652
 ; REFERENCE/DOCKET NUMBER: 6109, US.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 847-937-9803
 ; TELEFAX: 847-938-2623
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 490 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; 8-912-129A-50
 ;
 ; Query Match 89.0%; Score 113; DB 2; Length 490;
 ; Best Local Similarity 81.8%; Pred. No. 1.2e-08;
 ; Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 ;
 ; QY 1 LLSWGCKGRIVCTSVQNMET 22
 ; Db 372 LLLNMGCKGRILCYTSVKNMET 393
 ;
 ; RESULT 10
 ; US-08-912-129A-54
 ; Sequence 54, Application US/08912129A
 ; Patent No. 5922533
 ; GENERAL INFORMATION:
 ; APPLICANT: VALLARI, ANADRUZELA S.
 ; APPLICANT: HACKETT, JOHN JR.
 ; APPLICANT: HICKMAN, ROBERT K.
 ; APPLICANT: VARITEK, VINCENT A. JR.
 ; APPLICANT: NECKLAWS, ELIZABETH A.
 ; APPLICANT: GOLDEN, ALAN M.
 ; APPLICANT: BRENNAN, CATHERINE A.
 ; APPLICANT: DEVARE, SUSHIL G.
 ; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION

NUMBER OF SEQUENCES: 89
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 ; OPERATING SYSTEM: MS-DOS (Windows 95)
 ; SOFTWARE: Microsoft Word (ASCII format output)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/912,129A
 ; FILING DATE: 15-AUG-1997
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Danckers, Andreas M.
 ; REGISTRATION NUMBER: 32,652
 ; REFERENCE/DOCKET NUMBER: 6109, US.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 847-937-9803
 ; TELEFAX: 847-938-2623
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 618 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-912-129A-54
 ;
 ; Query Match 89.0%; Score 113; DB 2; Length 618;
 ; Best Local Similarity 81.8%; Pred. No. 1.6e-08;
 ; Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 ;
 ; QY 1 LLSWGCKGRIVCTSVQNMET 22
 ; Db 372 LLLNMGCKGRILCYTSVKNMET 393
 ;
 ; RESULT 11
 ; US-08-912-129A-61
 ; Sequence 61, Application US/08912129A
 ; Patent No. 5922533
 ; GENERAL INFORMATION:
 ; APPLICANT: VALLARI, ANADRUZELA S.
 ; APPLICANT: HACKETT, JOHN JR.
 ; APPLICANT: HICKMAN, ROBERT K.
 ; APPLICANT: VARITEK, VINCENT A. JR.
 ; APPLICANT: NECKLAWS, ELIZABETH A.
 ; APPLICANT: GOLDEN, ALAN M.
 ; APPLICANT: BRENNAN, CATHERINE A.
 ; APPLICANT: DEVARE, SUSHIL G.
 ; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
 ; NUMBER OF SEQUENCES: 89
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 ; OPERATING SYSTEM: MS-DOS (Windows 95)
 ; SOFTWARE: Microsoft Word (ASCII format output)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912.129A
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckers, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 873 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-912-129A-61

Query Match      89.0%; Score 113; DB 2; Length 873;
Best Local Similarity 81.8%; Pred. No. 2.2e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 601 LLSWGCKGRVLCYTSVQNMET 622

RESULT 12
US-09-433-428D-6
; Sequence 6, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leye, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CCS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-6

Query Match      87.4%; Score 111; DB 4; Length 33;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LLSWGCKGRVLCYTSVQNM 20
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Db 14 LLSWGCKGRVLCYTSVQNM 33

RESULT 13
US-09-433-428D-25
; Sequence 25, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leye, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CCS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-25

Query Match      86.6%; Score 110; DB 4; Length 33;
Best Local Similarity 90.0%; Pred. No. 2.1e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LLSWGCKGRVLCYTSVQNM 20
   ||:|||||:|||||:|||||
Db 14 LLSWGCKGRVLCYTSVQNM 33

RESULT 14
US-08-894-699-36
; Sequence 36, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-ARAKA, IBITISSAM
; APPLICANT: LY, THOI-DUONG
; APPLICANT: CHAIX-BUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSER: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-OBCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-36

Query Match      86.6%; Score 110; DB 3; Length 40;
Best Local Similarity 81.8%; Pred. No. 2.5e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Thu May 29 15:25:09 2003

us-09-147-362a-3.rai

Page 7

QY 1 LLSMCKGRLVCTSVQWNET 22
|:|||||:|||||:
Db 19 LLSMCKGRLVCTSVQWNET 40

RESULT 15
US-09-444-410-36

; Sequence 36, Application US/09444410
; Patent No. 6270975

; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS

; APPLICANT: SARAGOSTI, SENTOB

; APPLICANT: LOUSSEST-AJAKA, IBITISSAM

; APPLICANT: LY, THOAI-DUONG

; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

; ADDRESS: P. C.

; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/444,410

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/894,699

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95/02236

; FILING DATE: 27-FEB-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,614

; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-444-410-36

Query Match 86.6%; Score 110; DB 4; Length 40;

Best Local Similarity 81.8%; Pred. No. 2.5e-09;

Matches 18; Conservative 3; Mismatches 1; Indels 0;

Gaps 0;

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|:|||||:|||||:
Db 19 LLSMCKGRLVCTSVQWNET 40

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Job time : 9.95238 secs

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OM protein - protein search, using SW model

Run on: May 29, 2003, 10:39:21 ; Search time 19.0317 Seconds

(without alignments)
117.011 Million cell updates/sec

Title: US-09-147-362a-3

Perfect score: 127
Sequence: 1 L1SSWGCKGRIVCTSYQNMET 22

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Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 101223694 residues

1 number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA.*

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	89.0	215	1 US-08-911-824-58	Sequence 58, Appl
2	113	89.0	245	1 US-08-911-824-48	Sequence 48, Appl
3	113	89.0	281	1 US-08-911-824-120	Sequence 120, Appl
4	113	89.0	373	1 US-08-911-824-52	Sequence 52, Appl
5	113	89.0	460	1 US-08-911-824-60	Sequence 60, Appl
6	113	89.0	488	1 US-08-911-824-95	Sequence 95, Appl
7	113	89.0	490	1 US-08-911-824-50	Sequence 50, Appl
8	113	89.0	526	1 US-08-911-824-97	Sequence 97, Appl
9	113	89.0	618	1 US-08-911-824-54	Sequence 54, Appl
10	113	89.0	706	1 US-08-911-824-93	Sequence 93, Appl
11	113	89.0	736	1 US-08-911-824-91	Sequence 91, Appl
12	113	89.0	873	1 US-08-911-824-61	Sequence 61, Appl
13	109	85.8	37	9 US-10-026-741-86	Sequence 86, Appl
14	109	85.8	200	10 US-09-854-816-104	Sequence 104, Appl
15	106	83.5	37	9 US-10-026-741-94	Sequence 94, Appl
16	106	83.5	104	9 US-10-026-741-100	Sequence 100, Appl
17	103	81.1	35	9 US-10-026-741-101	Sequence 101, Appl
18	103	81.1	37	9 US-10-026-741-7	Sequence 7, Appl
19	103	81.1	37	9 US-10-026-741-90	Sequence 90, Appl

20	103	81.1	351	9 US-10-026-741-47	Sequence 47, Appl
21	103	81.1	877	9 US-10-026-741-102	Sequence 102, Appl
22	102	80.3	23	9 US-10-026-741-30	Sequence 30, Appl
23	101	79.5	37	9 US-10-026-741-88	Sequence 88, Appl
24	99	78.0	213	10 US-09-854-816-103	Sequence 103, Appl
25	96	75.6	23	9 US-09-388-847-4	Sequence 4, Appl
26	96	75.6	12	12 US-10-000-321-2	Sequence 2, Appl
27	96	75.6	24	9 US-10-026-741-34	Sequence 34, Appl
28	96	75.6	35	9 US-09-886-156-62	Sequence 62, Appl
29	96	75.6	35	9 US-09-886-150-62	Sequence 62, Appl
30	96	75.6	35	9 US-09-886-149-62	Sequence 62, Appl
31	96	75.6	35	9 US-09-886-159-62	Sequence 62, Appl
32	96	75.6	146	12 US-10-000-321-10	Sequence 10, Appl
33	96	75.6	204	10 US-09-854-816-105	Sequence 105, Appl
34	96	75.6	351	9 US-09-886-156-46	Sequence 46, Appl
35	96	75.6	351	9 US-09-886-150-46	Sequence 46, Appl
36	96	75.6	351	9 US-09-886-149-46	Sequence 46, Appl
37	96	75.6	351	9 US-09-886-159-46	Sequence 46, Appl
38	86	67.7	268	10 US-09-854-816-39	Sequence 39, Appl
39	84	66.1	37	9 US-10-026-741-84	Sequence 84, Appl
40	84	66.1	204	10 US-09-854-816-106	Sequence 106, Appl
41	82	64.6	198	10 US-09-854-816-81	Sequence 81, Appl
42	81	63.8	37	9 US-10-026-741-82	Sequence 82, Appl
43	81	63.8	198	10 US-09-854-816-77	Sequence 77, Appl
44	81	63.8	198	10 US-09-854-816-78	Sequence 78, Appl
45	81	63.8	198	10 US-09-854-816-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-08-911-824-58
Sequence 58, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Shail G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165, US-01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 58
LENGTH: 215
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURES:
OTHER INFORMATION: Encodes recombinant protein pCO-8PL
US-08-911-824-58
Query Match
Best Local Similarity 89.0%; Score 113; DB 1; Length 215;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 L1SSWGCKGRIVCTSYQNMET 22
Db 127 L1LTMWGCKGRILICTSYQNMET 148
RESULT 2
US-08-911-824-48
Sequence 48, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories

```

; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-9PL
; US-911-824-48

Query Match      89.0%; Score 113; DB 1; Length 245;
Best Local Similarity 81.8%; Pred. No. 8.7e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      1  LLSWGCKGRILVCTSVQNMET 22
Db      127  LNLWGCKGRILICTSVKMNMT 148

RESULT 3
US-08-911-824-120
; Sequence 120, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-15PL
; US-08-911-824-120

Query Match      89.0%; Score 113; DB 1; Length 281;
Best Local Similarity 81.8%; Pred. No. 9.9e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      1  LLSWGCKGRILVCTSVQNMET 22
Db      127  LNLWGCKGRILICTSVKMNMT 148

RESULT 4
US-08-911-824-52
; Sequence 52, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-11PL
; US-08-911-824-52

Query Match      89.0%; Score 113; DB 1; Length 373;
Best Local Similarity 81.8%; Pred. No. 1.3e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      1  LLSWGCKGRILVCTSVQNMET 22
Db      127  LNLWGCKGRILICTSVKMNMT 148

RESULT 5
US-08-911-824-60
; Sequence 60, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-6CKS
; US-08-911-824-60

Query Match      89.0%; Score 113; DB 1; Length 460;
Best Local Similarity 81.8%; Pred. No. 1.6e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      1  LLSWGCKGRILVCTSVQNMET 22
Db      372  LNLWGCKGRILICTSVKMNMT 393

RESULT 6
US-08-911-824-95
; Sequence 95, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-6CKS
; US-08-911-824-95

Query Match      89.0%; Score 113; DB 1; Length 460;
Best Local Similarity 81.8%; Pred. No. 1.6e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      1  LLSWGCKGRILVCTSVQNMET 22
Db      372  LNLWGCKGRILICTSVKMNMT 393
```

```

; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-15PL
; US-08-911-824-120

Query Match      89.0%; Score 113; DB 1; Length 281;
Best Local Similarity 81.8%; Pred. No. 9.9e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      1  LLSWGCKGRILVCTSVQNMET 22
Db      127  LNLWGCKGRILICTSVKMNMT 148

RESULT 4
US-08-911-824-52
; Sequence 52, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-11PL
; US-08-911-824-52

Query Match      89.0%; Score 113; DB 1; Length 373;
Best Local Similarity 81.8%; Pred. No. 1.3e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      1  LLSWGCKGRILVCTSVQNMET 22
Db      127  LNLWGCKGRILICTSVKMNMT 148

RESULT 5
US-08-911-824-60
; Sequence 60, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-6CKS
; US-08-911-824-60

Query Match      89.0%; Score 113; DB 1; Length 460;
Best Local Similarity 81.8%; Pred. No. 1.6e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      1  LLSWGCKGRILVCTSVQNMET 22
Db      372  LNLWGCKGRILICTSVKMNMT 393

RESULT 6
US-08-911-824-95
; Sequence 95, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-6CKS
; US-08-911-824-95

Query Match      89.0%; Score 113; DB 1; Length 460;
Best Local Similarity 81.8%; Pred. No. 1.6e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      1  LLSWGCKGRILVCTSVQNMET 22
Db      372  LNLWGCKGRILICTSVKMNMT 393
```

```

; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-14PL
US-08-911-824-95

```

```

Query Match      89.0%; Score 113; DB 1; Length 488;
Best Local Similarity 81.8%; Pred. No. 1.7e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LLSWGCKGRIVCTSYQNMET 22
Db 127 LNLWGCKGRILCTSYKMNMT 148

```

```

RESULT 7
US-08-911-824-50
; Sequence 50, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-9CKS
US-08-911-824-50

```

```

Query Match      89.0%; Score 113; DB 1; Length 490;
Best Local Similarity 81.8%; Pred. No. 1.7e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LLSWGCKGRIVCTSYQNMET 22
Db 372 LNLWGCKGRILCTSYKMNMT 393

```

```

RESULT 8
US-08-911-824-97
; Sequence 97, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.

```

```

; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-15CKS
US-08-911-824-97

```

```

Query Match      89.0%; Score 113; DB 1; Length 526;
Best Local Similarity 81.8%; Pred. No. 1.8e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LLSWGCKGRIVCTSYQNMET 22
Db 372 LNLWGCKGRILCTSYKMNMT 393

```

```

RESULT 9
US-08-911-824-54
; Sequence 54, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-11CKS
US-08-911-824-54

```

```

Query Match      89.0%; Score 113; DB 1; Length 618;
Best Local Similarity 81.8%; Pred. No. 2.1e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LLSWGCKGRIVCTSYQNMET 22
Db 372 LNLWGCKGRILCTSYKMNMT 393

```

```

RESULT 10
US-08-911-824-93
; Sequence 93, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.

```

APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 93
LENGTH: 706
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pGO-13CKS
US-08-911-824-93

Query Match 89.0%; Score 113; DB 1; Length 706;
Best Local Similarity 81.8%; Pred. No. 2.4e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCYTSVQNMET 22
||:|||||:|||||:
Db 618 LNLWGCKGRLICYTSVXNMET 639

RESULT 11
US-08-911-824-91
Sequence 91, Application US/08911824
Publication No. US2003004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 91
LENGTH: 736
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pGO-12CKS
US-08-911-824-91

Query Match 89.0%; Score 113; DB 1; Length 736;
Best Local Similarity 81.8%; Pred. No. 2.5e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCYTSVQNMET 22
||:|||||:|||||:
Db 618 LNLWGCKGRLICYTSVXNMET 639

RESULT 12
US-08-911-824-61
Sequence 61, Application US/08911824
Publication No. US2003004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.

APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 61
LENGTH: 873
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: HIV-1 Group O isolate HAM112
US-08-911-824-61

Query Match 89.0%; Score 113; DB 1; Length 873;
Best Local Similarity 81.8%; Pred. No. 2.9e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCYTSVQNMET 22
||:|||||:|||||:
Db 601 LNLWGCKGRLICYTSVXNMET 622

RESULT 13
US-10-026-741-86
Sequence 86, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
QUILLIENT, CAROLINE
GUETARD, DENISE
MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQUELINE
COHEN, JACQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunnet, Henderson, Farbow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 86:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 86:
 US-10-026-741-86

Query Match 85.8%; Score 109; DB 9; Length 37;
 Best Local Similarity 81.8%; Pred. No. 5.5e-09;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVCTSVQNMET 22
 14 LLSWGCKGRVCTSVQNMRT 35

RESULT 14
 9-854-816-104
 Sequence 104, Application US/09854816
 Patent No. US20020151473A1
 GENERAL INFORMATION:
 APPLICANT: Andrew C. Braisted
 J. Kevin Judice
 Robert S. McDowell
 J. Christopher Phelan
 Melissa A. Starovashnik
 James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/854,816
 FILING DATE: 15-May-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/965,056
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, PhD., Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: P1005R2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-8674
 TELEFAX: 650/953-9881
 INFORMATION FOR SEQ ID NO: 104:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 amino acids
 TYPE: Amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 104:
 US-09-854-816-104

Query Match 85.8%; Score 109; DB 10; Length 200;
 Best Local Similarity 81.8%; Pred. No. 2.7e-08;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVCTSVQNMET 22
 14 LLSWGCKGRVCTSVQNMRT 35

Db 126 LLSWGCKGRVCTSVQNMRT 147

RESULT 15
 US-10-026-741-94
 Sequence 94, Application US/10026741
 Publication No. US20030049604A1
 GENERAL INFORMATION:
 APPLICANT: CHARNEAU, PIERRE
 CLAVEL, FRANCOISE
 BORMAN, ANDREW
 OUILLET, CAROLINE
 GUERARD, DENISE
 MONTAGNIER, LUC
 DONON DE SAINT-MARTIN, JACQUELINE
 COHEN, JACQUES
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR SUBTYPE) ANTIGENS

NUMBER OF SEQUENCES: 103
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Flinnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/026,741
 FILING DATE: 27-Dec-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/817,441
 FILING DATE: 31-AUG-1998
 APPLICATION NUMBER: PCT/FR 95/01391
 FILING DATE: 20-OCT-1995
 APPLICATION NUMBER: FR 9412554
 FILING DATE: 20-OCT-1994
 APPLICATION NUMBER: FR 9502526
 FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 03260.6005-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 94:
 US-10-026-741-94

Query Match 83.5%; Score 106; DB 9; Length 37;
 Best Local Similarity 72.7%; Pred. No. 1.5e-08;
 Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVCTSVQNMET 22
 14 LLSWGCKGRVCTSVQNMRT 35

Search completed: May 29, 2003, 11:03:56
 Job time: 19.0317 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:06 ; Search time 10.8254 Seconds
(without alignments)
195.370 Million cell updates/sec

Title: US-09-147-362A-3

Perfect score: 127
Sequence: 1 LLSWGCKGRILVCTSVQNMNET 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	109	85.8	863	2 AS3034	gag polyprotein -
2	106	83.5	104	2 S52930	GP41 ENV protein -
3	103	81.1	877	2 S49197	envelope protein p
4	84	66.1	854	1 VCLJ81	env polyprotein pr
5	83	65.4	357	2 S21990	envelope protein g
6	83	65.4	358	2 S22002	envelope protein g
7	82	64.6	358	2 S22000	envelope protein g
8	82	64.6	358	2 S70417	envelope protein g
9	81	63.8	443	2 S41621	env polyprotein p
10	81	63.8	853	2 S54384	envelope polyprote
11	81	63.8	855	1 VCLJZR	env polyprotein pr
12	80	63.0	357	2 S22006	envelope protein g
13	80	63.0	357	2 S21994	envelope protein g
14	80	63.0	357	2 S22004	envelope protein g
15	80	63.0	357	2 S21996	envelope protein g
16	80	63.0	357	2 S21992	envelope protein g
17	80	63.0	358	2 S21998	envelope protein g
18	80	63.0	445	2 A41621	env polyprotein M
19	80	63.0	454	2 B41621	env polyprotein D
20	80	63.0	843	1 H44001	env polyprotein pr
21	80	63.0	847	2 T09448	envelope glycoprot
22	80	63.0	847	2 S13289	env protein - huma
23	80	63.0	852	1 VCLJBR	env polyprotein -
24	80	63.0	852	2 T12016	envelope glycoprot
25	80	63.0	854	2 S13288	env protein - huma
26	80	63.0	855	1 VCLJAZ	env polyprotein pr
27	80	63.0	856	1 VCLJH3	env polyprotein pr
28	80	63.0	856	1 VCLJVL	env polyprotein pr
29	80	63.0	856	1 VCLJ3W	env polyprotein pr

30	80	63.0	859	1 VCLJMN	env polyprotein pr
31	80	63.0	861	1 VCLJLV	env polyprotein pr
32	80	63.0	861	1 VCLJSC	env polyprotein pr
33	80	63.0	868	1 VCLJH4	env polyprotein -
34	79	62.2	786	2 S28084	env polyprotein -
35	78.5	61.8	855	2 A45713	Env transmembrane
36	78	61.4	856	2 A44963	env polyprotein pr
37	77	60.6	846	1 VCLJND	env polyprotein pr
38	74.5	58.7	859	1 VCLJST	env polyprotein pr
39	74.5	58.7	859	2 S24571	env protein - huma
40	74.5	58.7	885	2 S04322	env protein - huma
41	74.5	58.7	886	2 T11555	env protein - simi
42	74	58.3	729	1 VCLJXK	env polyprotein pr
43	74	58.3	861	1 VCLJXB	env polyprotein pr
44	73	57.5	851	2 S33985	env polyprotein -
45	72.5	57.1	151	2 S30448	env protein - huma

ALIGNMENTS

RESULT 1
A53034
gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: A53034
R:Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groen, J. Virol. 68, 1586-1596, 1994
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African hu
A:Reference number: A53034; MUID:94149849; PMID:8107220
A:Accession: A53034
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-863 <VAN>
A:Cross-references: GB:L02587
C:Superfamily: type B retrovirus env polyprotein
C:Keywords: polyprotein

Query Match 85.8%; Score 109; DB 2; Length 863;
Best Local Similarity 81.8%; Pred. No. 9.5e-08;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRILVCTSVQNMNET 22
Db 594 LLSWGCKGRILVCTSVQNMNET 615

RESULT 2

S52930
GP41 ENV protein - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C:Accession: S52930
R:Conen, J.H.M.; Guetard, D.; Philbert, F.; Chamares, S.; Tabery, T.; Montgnier, L.; de
submitted to the EMBL Data Library, January 1995
A:Description: A novel HIV-1 O strain illustrates the diversity of the O group.
A:Reference number: S52929
A:Accession: S52930
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-104 <COH>
A:Cross-references: EMBL:X84328; NID:G695526; PIDN:CA459066.1; PID:G695527
C:Superfamily: type E retrovirus env polyprotein

Query Match 83.5%; Score 106; DB 2; Length 104;
Best Local Similarity 72.7%; Pred. No. 4e-08;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRILVCTSVQNMNET 22
Db 45 LLSWGCKGRILVCTSVQNMNET 66

RESULT 3

S49197
envelope protein precursor - human immunodeficiency virus type 1 (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
C/Accession: S49197
R/Character: P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chameret, S.; Cohen, J.; Remy, submitted to the EMBL Data Library, July 1994
A/Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: def
A/Reference number: S49197
A/Accession: S49197
A/Molecule type: DNA
A/Residues: 1-877 <CHA>
A/Cross-references: EMBL:X80020; NID:G510516; PIDN:CAA56323.1; PID:G510517
A/Experimental source: Isolate VAV
C/Superfamily: type E retrovirus env polypotein
C/Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein
F/1-30/Domin: signal sequence #status predicted <Sig>
F/1-535/Product: coat protein gp120 #status predicted <CP1>
F/56-877/Product: coat protein gp41 #status predicted <CP2>
F/568-716/Domin: transmembrane #status predicted <TMN>
F/59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,

Query Match 81.1% Score 103; DB 2; Length 877;
Best Local Similarity 72.7% Pred. No. 6,9e-07;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQWNET 22
DB 607 LLNMGCKRRLICVTSVKWNT 628

RESULT 4

env polypotein precursor - simian immunodeficiency virus SIVCPZ
N/Alternate names: coat polypotein
N/Contains: coat protein gp120; coat protein gp41
C/Species: simian immunodeficiency virus SIVCPZ
A/Note: host Pan troglodytes (chimpanzee)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C/Accession: S09990
R/Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A/Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A/Reference number: S09993; MUID:90259077; PMID:2188136
A/Accession: S09990
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-854 <HUB>
A/Cross-references: EMBL:X52154; NID:G58866; PIDN:CAA36407.1; PID:G58874
C/Genetics:

A/Gene: env
C/Superfamily: type E retrovirus env polypotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein
F/1-30/Domin: signal sequence #status predicted <Sig>
F/31-500/Product: coat protein gp120 #status predicted <CP1>
F/501-854/Product: coat protein gp41 #status predicted <CP2>
F/501-517/Domin: transmembrane #status predicted <TM1>
F/567-653/Domin: transmembrane #status predicted <TM2>
F/805-821/Domin: transmembrane #status predicted <TM3>
F/133,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 66.1% Score 84; DB 1; Length 854;
Best Local Similarity 54.5% Pred. No. 0.00035;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQWNET 22
DB 582 ILGLMGCSGKAVCYTVPWNN 603

RESULT 5

S21990

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 20
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21990; S70423
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A/Reference number: S21990
A/Accession: S21990
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb
A/Reference number: S70417; MUID:92144209; PMID:11736940
A/Accession: S70423
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-332, 'X', 334-357 <STE2>
A/Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176
C/Superfamily: type E retrovirus env polypotein

Query Match 65.4% Score 83; DB 2; Length 357;
Best Local Similarity 65.0% Pred. No. 0.00023;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQWNET 20
DB 93 LLGLMGCSGRLICTTAVPWN 112

RESULT 6

envelope protein gp120/gp41 - human immunodeficiency virus type 1
S22002
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:G60186; PIDN:CAA43616.1; PID:G60187
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb
A/Reference number: S70417; MUID:92144209; PMID:11736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STE2>
A/Cross-references: EMBL:X61352; NID:G60186
C/Superfamily: type E retrovirus env polypotein

Query Match 65.4% Score 83; DB 2; Length 358;
Best Local Similarity 65.0% Pred. No. 0.00023;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQWNET 20
DB 94 LLGLMGCSGRLICTTAVPWN 113

RESULT 7

S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
 C/Accession: S22000
 R/Stculer, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 A/Submitted to the EMBL Data Library, July 1991
 A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
 A/Reference number: S21990
 A/Accession: S22000
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-358 <STE>
 A/Cross-references: EMBL:X61351
 C/Superfamily: type E retrovirus env polypotein

Query Match 64.6%; Score 82; DB 2; Length 358;
 Best Local Similarity 65.0%; Pred. No. 0.00031;
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRILVCYTSVQNM 20
 94 LLGIWCGSGRLICTTVPWN 113

RESULT 8
 S70417
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Valley: patient 3B
 C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
 C/Accession: S70417
 R/Stculer, H.; Storch-Hagenlocher, B.; Wildemann, B.
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb
 A/Reference number: S70417; MUID:92144209; PMID:1736940
 A/Accession: S70417
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-358 <STE>
 A/Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185
 C/Superfamily: type E retrovirus env polypotein

Query Match 64.6%; Score 82; DB 2; Length 358;
 Best Local Similarity 65.0%; Pred. No. 0.00031;
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRILVCYTSVQNM 20
 94 LLGIWCGSGRLICTTVPWN 113

RESULT 9
 C41621
 env polypotein P - human immunodeficiency virus type 1 (fragment)
 N/Alternate names: coat polypotein
 N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
 C/Accession: C41621
 R/Burger, H.; Weiser, B.; Flaheerty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
 A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A/Reference number: A41621; MUID:92107924; PMID:1763038
 A/Accession: C41621
 A/Molecule type: DNA
 A/Residues: 1-443 <BUR>
 A/Cross-references: GB:M77230; NID:9328631; PIDN:AA003792.1; PID:9555015
 A/Note: this virus was isolated from the mother's sexual partner
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polypotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypot
 F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:424-443/Domain: transmembrane #status predicted <TM>
 F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 63.8%; Score 81; DB 2; Length 443;
 Best Local Similarity 54.5%; Pred. No. 0.00053;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRILVCYTSVQNM 22
 332 LLGIWCGSGRLICTTAVPMNNS 353

RESULT 10
 S54384
 envelope polypotein - human immunodeficiency virus type 1
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
 C/Accession: S54384
 R/Theodore, T.; Buckler-White, A.J.
 A/Submitted to the EMBL Data Library, July 1989
 A/Reference number: S54377
 A/Accession: S54384
 A/Status: preliminary
 A/Molecule type: genomic RNA
 A/Residues: 1-853 <THE>
 A/Cross-references: EMBL:M22639; NID:9329377; PIDN:AAA45370.1; PID:9329385
 C/Superfamily: type E retrovirus env polypotein
 C/Keywords: polypotein

Query Match 63.8%; Score 81; DB 2; Length 853;
 Best Local Similarity 54.5%; Pred. No. 0.00093;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRILVCYTSVQNM 22
 589 LLGIWCGSGRLICTTVPNMNS 610

RESULT 11
 VCL12R
 env polypotein precursor - human immunodeficiency virus Zr-6
 N/Alternate names: coat polypotein
 C/Species: human immunodeficiency virus Zr-6
 C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
 C/Accession: D26192
 R/Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Peorino, P.; Schochetman, G.; Cu
 Gene 52, 71-82, 1987
 A/Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti
 A/Reference number: A26192; MUID:87248097; PMID:3036660
 A/Accession: D26192
 A/Molecule type: DNA
 A/Residues: 1-855 <SRI>
 A/Cross-references: GB:K03458; GB:M16322; NID:9329398; PIDN:AAA45380.1; PID:9329403
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polypotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypot
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-855/Product: env polypotein #status predicted <MNT>
 F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
 F:501-855/Product: transmembrane glycoprotein #status predicted <TM>
 F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 63.8%; Score 81; DB 1; Length 855;
 Best Local Similarity 54.5%; Pred. No. 0.00093;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRILVCYTSVQNM 22
 591 LLGIWCGSGRLICTTVPNMNS 612

RESULT 12

S22006
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S70420; S22006
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70420
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A:Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
 A:Experimental source: patient L
 A>Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 63.0%; Score 80; DB 2; Length 357;
 Best Local Similarity 60.0%; Pred. No. 0.0006;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVCTTSVQWN 20
 DB 93 LLGIWCGSGKLICTTAVPMN 112

RESULT 13
 S21994
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C:Accession: S21994; S70421
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
 A:Reference number: S21990
 A:Accession: S21994
 A:Molecule type: DNA
 A:Residues: 1-357 <STB1>
 A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70421
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STB2>
 A:Cross-references: EMBL:X61355; NID:g60179
 C:Superfamily: type E retrovirus env polyprotein

Query Match 63.0%; Score 80; DB 2; Length 357;
 Best Local Similarity 60.0%; Pred. No. 0.0006;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVCTTSVQWN 20
 DB 93 LLGIWCGSGKLICTTAVPMN 112

RESULT 14
 S22004
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Variety: isolate 4B
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C:Accession: S22004; S70419
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
 A:Reference number: S21990

A:Accession: S22004
 A:Molecule type: DNA
 A:Residues: 1-357 <STB1>
 A:Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70419
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-292, 'X', 294-357 <STB2>
 A:Cross-references: EMBL:X61353; NID:g60188
 C:Superfamily: type E retrovirus env polyprotein

Query Match 63.0%; Score 80; DB 2; Length 357;
 Best Local Similarity 60.0%; Pred. No. 0.0006;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVCTTSVQWN 20
 DB 93 LLGIWCGSGKLICTTAVPMN 112

RESULT 15
 S21996
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S70422; S21996
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70422
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129
 A:Experimental source: patient 27L
 A>Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 63.0%; Score 80; DB 2; Length 357;
 Best Local Similarity 60.0%; Pred. No. 0.0006;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVCTTSVQWN 20
 DB 93 LLGIWCGSGKLICTTAVPMN 112

Search completed: May 29, 2003, 10:40:23
 Job time: 10.8254 secs


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FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 854 AA; 95803 MW; 28249AFAD4F2D983 CRC64;

Query March 66.1%; Score 84; DB 1; Length 854;
Best Local Similarity 54.5%; Pred. No. 3.4e-05;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 L1SSWGCKGRIVCTSYQVNMET 22
582 ILGLMGCSGKAVCYTTPVNMNS 603

RESULT 2
ENV_HV122 STANDARD; PRT; 853 AA.
ID ENV_HV122
AC P12487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Z2/CDC-Z34 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M2639; AAA45370.1; -.
DR HIV; M2639; ENV52226.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 330 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B08BCBAFF7008 CRC64;

Query March 63.8%; Score 81; DB 1; Length 853;
Best Local Similarity 54.5%; Pred. No. 9.8e-05;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 L1SSWGCKGRIVCTSYQVNMET 22
589 ILGLMGCSGKILCTTTPVNMNS 610

RESULT 3
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; Pubmed=303660;
RA Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
RA Schoeneman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from
RT zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene."
RL Gene 52:71-82(1987).
CC -----
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CC -----
CC EMBL; K03458; AAA45380.1; -.
DR PIR; D26192; VCLDZR.

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DR HIV, K03458; ENV526.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120, 1.
 DR Pfam; PF00517; GP41, 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 30
 FT CHAIN 51 510
 FT CHAIN 511 855
 FT DISULFID 53 73
 FT DISULFID 118 207
 FT DISULFID 125 198
 FT DISULFID 130 155
 FT DISULFID 220 249
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 FT DISULFID 378 444
 FT DISULFID 385 417
 FT CARBOHYD 87 87
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 FT CARBOHYD 140 140
 FT CARBOHYD 145 145
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 FT CARBOHYD 673 673
 SQ SEQUENCE 855 AA; 96971 MW; 384D3D6E339C457 CRC64;
 Query Match 63.8%; Score 81; DB 1; Length 855;
 Best Local Similarity 54.5%; Pred. No. 9.8e-05;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LLSWGCKGLVYTSVQWNET 22
 Db 591 LLGIWGGGKRLCTTVPMNNS 612
 RESULT 4
 ID ENV_HV1Y2 STANDARD; PRT; 843 AA.
 AC P35561;
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).

OC Viruses; Retroviridae; Lentivirus.
 OX NCBI TaxID=36377;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9302387; PubMed=1404605;
 RA Li Y., Hui H., Burgess C.U., Price R.W., Sharp P.M., Hahn B.H.,
 Shaw G.M.;
 RT "Complete nucleotide sequence, genome organization, and biological
 properties of human immunodeficiency virus type 1 in vivo: evidence
 for limited defectiveness and complementation.";
 RL J. Virol. 66:6587-6600(1992).
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M93258; NOT_ANNOTATED_CDS.
 DR PIR; H44001; H44001.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120, 1.
 DR Pfam; PF00517; GP41, 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 489
 FT CHAIN 490 843
 FT TRANSMEM 738 755
 FT DISULFID 53 73
 FT DISULFID 118 201
 FT DISULFID 125 192
 FT DISULFID 130 155
 FT DISULFID 214 243
 FT DISULFID 224 235
 FT DISULFID 292 326
 FT DISULFID 373 432
 FT DISULFID 380 405
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
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 FT CARBOHYD 138 138
 FT CARBOHYD 154 154
 FT CARBOHYD 158 158
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 SQ SEQUENCE 843 AA; 95648 MW; C69PDD971C918B71 CRC64;
 Query Match 63.0%; Score 80; DB 1; Length 843;
 Best Local Similarity 60.0%; Pred. No. 0.00014;

Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSSMGCKGRVCTYSQVN 20
Db 579 LLAGMGCGSKLCTTAVPMN 598

RESULT 5
ENV_HV1S1 STANDARD; PRT; 847 AA.

AC P19550;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
NCBI_TaxID=11691;
(1)

RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398 (1990).

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CC EMBL: M65024; AAA5072.1; -
DR HIV; M38428; ENVSSP162.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
FT SIGNAL. 1 29
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 503 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 847 AA; 96135 MW; 0A901317DFEF2AB CRC64;

Query Match 63.0%; Score 80; DB 1; Length 847;
Best Local Similarity 60.0%; Pred. No. 0.00014;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSSMGCKGRVCTYSQVN 20
Db 583 LLAGMGCGSKLCTTAVPMN 602

RESULT 6
ENV_HV1W2 STANDARD; PRT; 847 AA.

AC P05680;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (MMJ2 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
NCBI_TaxID=11705;
(1)

RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RT Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or at risk for AIDS.";
RL Science 232:1548-1553 (1986).
CC -1- MISCELLANEOUS: ISOLATES MMJ1, MMJ2, AND MMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

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CC EMBL: M12507; AAB1290.1; -
DR HIV; M12507; ENV\$MMJ2.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
FT SIGNAL. 1 29
FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 502 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 202 BY SIMILARITY.
FT DISULFID 125 193 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 225 236 BY SIMILARITY.
FT DISULFID 293 326 BY SIMILARITY.
FT DISULFID 372 435 BY SIMILARITY.
FT DISULFID 379 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96466 MW; CDIE33D73A5B5CAE CRC64;

Query Match 63.0%; Score 80; DB 1; Length 847;
 Best Local Similarity 60.0%; Pred. No. 0.00014;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCYTSVQNM 20
 Db 583 LLSWGCKGRIVCYTSVQNM 602

RESULT 7
 ENV_HV1B8 STANDARD; PRT; 851 AA.
 AC P04582; (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 ENV.

Human immunodeficiency virus type 1 (B8 isolate) (HIV-1).
 Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11684;

SEQUENCE FROM N.A.

RA MEDLINE=8511123; PubMed=2578615;
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Stargich B.R.,
 RA Joseph S.F., Doran E.R., Rafalski J.A., Whitcomb E.A.,
 RA Baumbach K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
 RA Laubenstein J.A., Papas T.S., Chirayab J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RL Nature 313:277-284 (1985).

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 CC or send an email to license@isb-sib.ch).

DR EMBL; K02011; AAA44661.1; -
 DR HIV; K02011; ENV5B8;
 DR GlycoSuiteDB; P04582; -

DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 506
 FT CHAIN 507 851
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 440
 FT DISULFID 385 413
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
 FT CARBOHYD 339 339
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 401 401
 FT CARBOHYD 443 443
 FT CARBOHYD 458 458
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 FT CARBOHYD 611 611
 FT CARBOHYD 620 620
 FT CARBOHYD 632 632
 FT CARBOHYD 669 669
 FT CARBOHYD 745 745
 FT CARBOHYD 811 811
 SQ SEQUENCE 851 AA; 96444 MW; D16A3C9857785F1 CRC64;

Query Match 63.0%; Score 80; DB 1; Length 851;
 Best Local Similarity 60.0%; Pred. No. 0.00014;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCYTSVQNM 20
 Db 587 LLSWGCKGRIVCYTSVQNM 606

RESULT 8

ENV_HV1B8

ENV_HV1B8 STANDARD; PRT; 852 AA.

AC P12488;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

ENV.

Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).

Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11693;

SEQUENCE FROM N.A.

Query Match	Best Local Similarity	63.0%	Score 80;	DB 1;	Length 852;
Matches 12;	Conservative 3;	Mismatches 5;	Indels 0;	Gaps 0;	
RA	MEDLINE=89085613; PubMed=2789516;				
RA	Andrad R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,				
RA	Dandekar S.,				
RT	"Biological and molecular characterization of human immunodeficiency				
RT	virus (HIV-1BR) from the brain of a patient with progressive				
RT	dementia".				
RL	Virology 168:79-89(1989).				
CC	-1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS				
CC	HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; M21098; AAA44221.1; -.				
DR	PIR; A11667; VCLJBR.				
DR	HIV; M21098; ENV5BRVA.				
DR	InterPro; IPR000328; Env GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00515; GP120.1.				
DR	Pfam; PF00517; GP41.1.				
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;				
KW	Signal.				
FT	CHAIN 1 30				
FT	CHAIN 31 507				
FT	CHAIN 508 852				
FT	DISULFID 54 74				
FT	DISULFID 119 205				
FT	DISULFID 126 196				
FT	DISULFID 131 155				
FT	DISULFID 218 247				
FT	DISULFID 228 239				
FT	DISULFID 296 330				
FT	DISULFID 376 439				
FT	DISULFID 383 412				
FT	CARBOHYD 49 49				
FT	CARBOHYD 88 88				
FT	CARBOHYD 135 135				
FT	CARBOHYD 138 138				
FT	CARBOHYD 154 154				
FT	CARBOHYD 158 158				
FT	CARBOHYD 197 197				
FT	CARBOHYD 234 234				
FT	CARBOHYD 241 241				
FT	CARBOHYD 262 262				
FT	CARBOHYD 276 276				
FT	CARBOHYD 289 289				
FT	CARBOHYD 295 295				
FT	CARBOHYD 301 301				
FT	CARBOHYD 331 331				
FT	CARBOHYD 354 354				
FT	CARBOHYD 360 360				
FT	CARBOHYD 384 384				
FT	CARBOHYD 390 390				
FT	CARBOHYD 396 396				
FT	CARBOHYD 400 400				
FT	CARBOHYD 442 442				
FT	CARBOHYD 456 456				
FT	CARBOHYD 607 607				
FT	CARBOHYD 612 612				
FT	CARBOHYD 621 621				
FT	CARBOHYD 633 633				
FT	CARBOHYD 670 670				
FT	CARBOHYD 812 812				
SO	SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;				

ID	ENV	HV1S3	STANDARD	PR	852 AA
DT	01-FEB-1991	(Rel. 17, Created)			
DT	01-FEB-1991	(Rel. 17, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (SF3 isolate) (HIV-1).				
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11690;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90317906; PubMed=2370688;				
RA	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;				
RT	"Human immunodeficiency virus type 1 cellular host range,				
RT	replication, and cytopathicity are linked to the envelope region of				
RT	the viral genome.";				
RL	J. Virol. 64:4016-4020(1990).				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; M38427; AAA45067.1; -.				
DR	HIV; M38427; ENVSEF33.				
DR	InterPro; IPR000328; Env GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120; 1.				
DR	Pfam; PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;				
KW	Signal.				
FT	SIGNAL.	1	31		
FT	CHAIN	32	506		
FT	CHAIN	507	852		
FT	DISULFID	53	73		
FT	DISULFID	118	206		
FT	DISULFID	125	197		
FT	DISULFID	130	156		
FT	DISULFID	219	248		
FT	DISULFID	229	240		
FT	DISULFID	297	331		
FT	DISULFID	377	439		
FT	DISULFID	384	412		
FT	CARBOHYD	87			
FT	CARBOHYD	129	129		
FT	CARBOHYD	136	136		
FT	CARBOHYD	141	141		
FT	CARBOHYD	142	142		
FT	CARBOHYD	155	155		
FT	CARBOHYD	159	159		
FT	CARBOHYD	189	189		
FT	CARBOHYD	198	198		
FT	CARBOHYD	242	242		
FT	CARBOHYD	263	263		
FT	CARBOHYD	277	277		
FT	CARBOHYD	290	290		
FT	CARBOHYD	296	296		
FT	CARBOHYD	332	332		
FT	CARBOHYD	339	339		
FT	CARBOHYD	355	355		

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FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 852 AA; 96663 MW; E7BBF8D23C9910D CRC64;

Query Match 63.0%; Score 80; DB 1; Length 852;
Best Local Similarity 60.0%; Pred. No. 0.00014;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 LLSWGCKGRVLCYTSVQWN 20
588 LLSWGCKGRVLCYTSVQWN 607

RESULT 10
ENV_HV1MF STANDARD; PRT; 853 AA.
AC P19551;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
Wasiak A.;
RT "Cloning and characterization of human immunodeficiency virus type 1
variants diminished in the ability to induce syncytium-independent
cytolysis.";
RL J. Virol. 64:3792-3803(1990).
CC -----
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CC -----
CC EMBL: M33943; AAA44850.1; -
DR HIV; M33943; ENVSMFA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 30
FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 203 BY SIMILARITY.
FT DISULFID 126 194 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 329 BY SIMILARITY.
FT DISULFID 376 443 BY SIMILARITY.

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FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 185 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 853 AA; 96912 MW; 337B993B6F22ABA CRC64;

Query Match 63.0%; Score 80; DB 1; Length 853;
Best Local Similarity 60.0%; Pred. No. 0.00014;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 LLSWGCKGRVLCYTSVQWN 20
590 LLSWGCKGRVLCYTSVQWN 609

RESULT 11
ENV_HV1A2 STANDARD; PRT; 855 AA.
ID ENV_HV1A2
AC P03378;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steiner K.S.,
Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
(ARV-2)."
RL Science 227:484-492(1985).
CC -----
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CC -----
CC EMBL: K02007; AAB59882.1; -

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DR PIR, A03976; VCLJ2A2.
 DR HIV, K02007; ENV5SF2.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120, 1.
 DR Pfam: PF00517; GP41, 1.
 DR A10S; Coat protein; Glycoprotein; Transmembrane; Signal.
 KW A10S; Coat protein; Glycoprotein; Transmembrane; Signal.
 FT CHAIN 1 29
 FT CHAIN 30 509
 FT CHAIN 510 855
 FT DISULFID 53 73
 FT DISULFID 118 208
 FT DISULFID 125 199
 FT DISULFID 130 155
 FT DISULFID 221 250
 FT DISULFID 231 242
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 FT CARBOHYD 87 87
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 FT CARBOHYD 140 140
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 FT CARBOHYD 158 158
 FT CARBOHYD 184 184
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 FT CARBOHYD 244 244
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 FT CARBOHYD 279 279
 FT CARBOHYD 292 292
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 FT CARBOHYD 400 400
 FT CARBOHYD 408 408
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 FT CARBOHYD 458 458
 FT CARBOHYD 461 461
 FT CARBOHYD 610 610
 FT CARBOHYD 615 615
 FT CARBOHYD 624 624
 FT CARBOHYD 636 636
 FT CARBOHYD 815 815
 SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC1A2 CRC64;

Query Match 63.0%; Score 80; DB 1; Length 855;
 Best Local Similarity 60.0%; Pred. No. 0.00014;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 LLSWGCGRVCTYSQVN 20
 591 LIGWCGSKLICTTAVPN 610

RESULT 12
 ENV_HV10Y STANDARD; PRT; 855 AA.
 AC P20B88;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor (Combats: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN ENV.
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).

CC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148544; PubMed=259749;
 RA Hueb T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot."
 RL AIDS 3:707-715(1989).
 CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
 CC HEALTHY GABONESE INDIVIDUAL.
 CC -----
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 CC -----
 DR EMBL: M26727; AAA83397.1; -.
 DR HIV, M26727; ENV5OY1.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120, 1.
 DR Pfam: PF00517; GP41, 1.
 DR A10S; Coat protein; Glycoprotein; Transmembrane; Signal.
 KW A10S; Coat protein; Glycoprotein; Transmembrane; Signal.
 FT CHAIN 1 29
 FT CHAIN 30 509
 FT CHAIN 510 855
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
 FT DISULFID 381 442
 FT DISULFID 388 415
 FT CARBOHYD 87 87
 FT CARBOHYD 134 134
 FT CARBOHYD 142 142
 FT CARBOHYD 145 145
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
 FT CARBOHYD 192 192
 FT CARBOHYD 202 202
 FT CARBOHYD 239 239
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
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 FT CARBOHYD 336 336
 FT CARBOHYD 359 359
 FT CARBOHYD 389 389
 FT CARBOHYD 395 395
 FT CARBOHYD 399 399
 FT CARBOHYD 405 405
 FT CARBOHYD 458 458
 FT CARBOHYD 610 610
 FT CARBOHYD 615 615
 FT CARBOHYD 624 624
 FT CARBOHYD 636 636
 FT CARBOHYD 815 815
 SQ SEQUENCE 855 AA; 97476 MW; 9C682A607AD62DA CRC64;

Query Match 63.0%; Score 80; DB 1; Length 855;
 Best Local Similarity 60.0%; Pred. No. 0.00014;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Thu May 29 15:25:19 2003

us-09-147-362a-3.rsp

Page 11

Query Match 63.0%; Score 80; DB 1; Length 856;
Best Local Similarity 60.0%; Pred. No. 0.00014;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 LLSWGCKGRIVCYTSVQWN 20
||| ||| :|: |||
Db 592 LLSWGCKGRIVCYTSVQWN 611

Search completed: May 29, 2003, 10:36:58
Job time : 5.4127 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:32:35 ; Search time 22.6984 Seconds
(without alignments)
199,707 Million cell updates/sec

Title: US-09-147-362a-3

Perfect score: 127

Sequence: 1 LLSWGCKGRILVCTSVQNMET 22

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mnc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP virus: *
16: SP bacteriophage: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	94.5	216	15	Q9IEC5 human immun
2	116	91.3	209	15	Q9IEB6 human immun
3	115	90.6	219	15	Q9IEB6 human immun
4	113	89.0	116	15	O40458 human immun
5	113	89.0	124	15	Q9IHU7 human immun
6	113	89.0	130	15	Q9IHU9 human immun
7	113	89.0	218	15	Q9IEB5 human immun
8	113	89.0	230	15	Q9IEB2 human immun
9	113	89.0	536	15	Q9IEB5 human immun
10	113	89.0	538	15	Q9IEB5 human immun
11	113	89.0	872	15	Q8Q7B0 human immun
12	113	89.0	879	15	Q9WIU9 human immun
13	113	89.0	880	15	Q8Q7H1 human immun
14	113	89.0	882	15	Q8Q7P9 human immun
15	113	89.0	887	15	Q8Q7H6 human immun
16	113	89.0	887	15	Q8Q7G9 human immun

17	113	89.0	900	15	Q9QNZ8 human immun
18	112	88.2	216	15	Q9IEC7 human immun
19	112	88.2	535	15	Q9IEF2 human immun
20	111	87.4	125	15	Q9IHU8 human immun
21	111	87.4	135	15	Q9IDOL9 human immun
22	111	87.4	230	15	Q9IEA9 human immun
23	111	87.4	242	15	Q9IEF31 human immun
24	111	87.4	529	15	Q9IEE2 human immun
25	110	86.6	114	15	O40448 human immun
26	110	86.6	116	15	O40459 human immun
27	110	86.6	137	15	Q9IHV5 human immun
28	110	86.6	172	15	Q9IEB3 human immun
29	110	86.6	177	15	Q9IEB0 human immun
30	110	86.6	208	15	Q9IEA3 human immun
31	110	86.6	219	15	Q9IEC8 human immun
32	110	86.6	227	15	Q9IEB9 human immun
33	110	86.6	234	15	Q9IEC2 human immun
34	110	86.6	342	15	O11942 human immun
35	110	86.6	418	15	O36547 human immun
36	110	86.6	502	15	Q9IEE3 human immun
37	110	86.6	871	15	O57074 human immun
38	110	86.6	871	15	O8Q7I2 human immun
39	110	86.6	876	15	O8Q7H3 human immun
40	109	85.8	114	15	O40456 human immun
41	109	85.8	114	15	O40472 human immun
42	109	85.8	118	15	O40451 human immun
43	109	85.8	213	15	Q9IEC4 human immun
44	109	85.8	214	15	Q9DIK3 human immun
45	109	85.8	225	15	Q9IEA0 human immun

ALIGNMENTS

RESULT 1

Q9IEC5 PRELIMINARY; PRT; 216 AA.
ID Q9IEC5;
AC Q9IEC5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF07;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT Philippe M.;
RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
DR EMBL; AJ236394; CAB96243.1;
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER
FT NON_TER
SQ SEQUENCE 216 AA; 25027 MW; 413AE9BFF1B4FC9A CRC64;

Query Match 94.5%; Score 120; DB-15; Length 216;
Best Local Similarity 90.9%; Pred. No. 9.6e-11;
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRILVCTSVQNMET 22
Db 47 LLSWGCKGRILVCTSVQNMET 68

RESULT 2
ID Q9IEB6 PRELIMINARY; PRT; 209 AA.

```
AC Q9IE66: 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Env polypeptide, gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BCF107;
RA Roques P., Robertson D., Darnaud F., Souquiere S., Mauciere P.,
RA Depienne C., Brun-Vezinet F., Dormont D., Simon F.O.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1."
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ238862; CAB96300.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 24116 MW; 91AC9B2BF74B83 CRC64;

Query Match
Best Local Similarity 91.3%; Score 116; DB 15; Length 209;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQNMET 22
DB 56 LLSWGCKGRIVCYTSVQNMET 77

RESULT 3
O9IEB6 PRELIMINARY; PRT; 219 AA.
ID Q9IEB6: 01-OCT-2000 (TReMBLrel. 15, Created)
AC Q9IEB6: 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BCF14;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (Jan-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ236404; CAB96252.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

Query Match
Best Local Similarity 90.6%; Score 115; DB 15; Length 219;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQNMET 22
DB 57 LLSWGCKGRIVCYTSVQNMET 78

RESULT 4
O40458 PRELIMINARY; PRT; 116 AA.
ID O40458
AC O40458;
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DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Envelope transmembrane glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=GROUP O;
RA Bibollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;
RT "Molecular characterization of envelope transmembrane glycoprotein of
RT 14 new human immunodeficiency virus type 1 group O strains from
RT different African countries."
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y09774; CAA70913.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 13865 MW; 540F5B3B7AD849D8 CRC64;

Query Match
Best Local Similarity 89.0%; Score 113; DB 15; Length 116;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQNMET 22
DB 39 LLSWGCKGRIVCYTSVQNMET 60

RESULT 5
O9IHU7 PRELIMINARY; PRT; 124 AA.
ID O9IHU7: 01-OCT-2000 (TReMBLrel. 15, Created)
AC O9IHU7: 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=97CM768;
RX MEDLINE=20386754; PubMed=10933623;
RA Yang C., Gao F., Fontjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O."
RL AIDS Res. Hum. Retroviruses 16:1075-1081 (2000).
DR EMBL; AF229237; AAF71914.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 15187 MW; 105D515F114450F8 CRC64;

Query Match
Best Local Similarity 89.0%; Score 113; DB 15; Length 124;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQNMET 22
DB 33 LLSWGCKGRIVCYTSVQNMET 54

RESULT 6
O9IHU9 PRELIMINARY; PRT; 130 AA.
ID O9IHU9
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AC 091HU9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN GP41.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97CM798;
 RX MEDLINE=20386754; PubMed=10933623;
 RA Yang C., Gao F., Ponjuno P.N., Zekeng L., van der Groen G.,
 Pleniak D., Schable C., Lal R.B.;
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV
 type 1 group O.";
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
 DR EMBL; AF229235; AAF1912.1;
 InterPro; IPR000328; Env_GP41.
 Pfam; PF00517; GP41; 1.
 Transmembrane.
 FT NON_TER 1 1
 SQ SEQUENCE 130 AA; 15593 MW; 5385789A336344EA CRC64;

Query Match 89.0%; Score 113; DB 15; Length 130;
 Best Local Similarity 81.8%; Pred. No. 7e-10;
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRLVCTSVQNMET 22
 Db 40 LLSWGCKGRLVCTSVQNMET 61

RESULT 7

AC 091EB5; PRELIMINARY; PRT; 218 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GP41 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YBF51;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 Philippe M.;
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ236425; CAB96273.1;
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 DR Transmembrane.
 FT NON_TER 1 1
 SQ SEQUENCE 218 AA; 25243 MW; E7F0E1E20EF79FA8 CRC64;

Query Match 89.0%; Score 113; DB 15; Length 218;
 Best Local Similarity 81.8%; Pred. No. 1.2e-09;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRLVCTSVQNMET 22
 Db 54 LLSWGCKGRLVCTSVQNMET 75

RESULT 8

O91EB2

ID 091EB2; PRELIMINARY; PRT; 230 AA.
 AC 091EB2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GP41 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YBF15;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 Philippe M.;
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ236408; CAB96256.1;
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 DR Transmembrane.
 FT NON_TER 1 1
 SQ SEQUENCE 230 AA; 26705 MW; C1F744F82F51302D CRC64;

Query Match 89.0%; Score 113; DB 15; Length 230;
 Best Local Similarity 81.8%; Pred. No. 1.2e-09;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRLVCTSVQNMET 22
 Db 55 LLSWGCKGRLVCTSVQNMET 76

RESULT 9

AC 091EB5; PRELIMINARY; PRT; 536 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Env polypeptide (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YBF15;
 RA Roques P., Robertson D., Damond F., Sousquiere S., Mauciere P.,
 Degienne C., Brun-Vezinet F., Dormont D.;
 RT "HIV-1 group O phylogenetic analysis of C2-gp41 region.";
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ133062; CAB96223.1;
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 1 1
 SQ SEQUENCE 536 AA; 60419 MW; 0F533ABAF08FE552 CRC64;

Query Match 89.0%; Score 113; DB 15; Length 536;
 Best Local Similarity 81.8%; Pred. No. 2.8e-09;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRLVCTSVQNMET 22
 Db 361 LLSWGCKGRLVCTSVQNMET 382

RESULT 10

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Q9IED5 ID Q9IED5 PRELIMINARY; PRT; 538 AA.
AC Q9IED5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BF51;
RA Roques P., Brun-Vezinet F., Dormont D.,
RA Deleporte E., Brun-Vezinet F., Dormont D.,
RT "HIV-1 group O phylogenetic analysis of C2-GP41 region."
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL, AJ133072; CAB6233.1; -.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT 538 1
SQ SEQUENCE 538 AA; 60777 MW; B3C9E66A233FEFID CRC64;

Query Match 89.0%; Score 113; DB 15; Length 538;
Best Local Similarity 81.8%; Pred. No. 2, 8e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVLYCTSVQWNET 22
DB 374 LLSWGCKGRVLYCTSVQWNET 395

RESULT 11
ID Q8Q7H0 PRELIMINARY; PRT; 872 AA.
AC Q8Q7H0;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CMA453;
RX MEDLINE=21849375; PubMed=11860674;
RA Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kaput L.,
RA Ngansop C., Zekeng L., Gurtler L.G., Devare S.G., Brennan C.A.;
RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
RT Phylogenetic Clusters."
RL AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL, AF383251; AAL98873.1; -.
SQ SEQUENCE 872 AA; 98344 MW; 91D37F6053827E3 CRC64;

Query Match 89.0%; Score 113; DB 15; Length 872;
Best Local Similarity 81.8%; Pred. No. 4, 5e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVLYCTSVQWNET 22
DB 602 LLSWGCKGRVLYCTSVQWNET 623

RESULT 12
Q9WU9 ID Q9WU9 PRELIMINARY; PRT; 879 AA.

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AC Q9WU9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp160 precursor.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VI686;
RX MEDLINE=99223950; PubMed=10207543;
RA Janssens W., Heyndrickx L., Van der Auwera G., Nkengasong J.,
RA Belinnet E., Vereecken K., Coppens S., Willems B., Franssen K.,
RA Peeters M., Ndunde P., Delaporte E., Van der Groen G.;
RT "Interpatient genetic variability of HIV-1 group O."
RL AIDS 13:41-48(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VI686;
RX MEDLINE=96426454; PubMed=8828748;
RA Delaporte E., Janssens W., Peeters M., Buve A., Dibanga G.,
RA Perret J.L., Ditsabou V., Georges Coubot M.C., Georges A.,
RA Bourgeois A., Samb B., Henzel D., Heyndrickx L., Franssen K.,
RA Van der Groen G., Larouz B., Mbe J.R.;
RT "Epidemiological and Molecular characteristics of HIV infection in
RT Gabon (1986 - 1994)."
RL AIDS 10:903-910(1996).
DR EMBL, X96526; CA65373.1; -.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Signal; Transmembrane.
FT SIGNAL 1
FT CHAIN 30 524 POTENTIAL.
FT CHAIN 132 156 V1.
FT CHAIN 164 200 V2.
FT CHAIN 302 335 V3.
FT CHAIN 395 427 V4.
FT CHAIN 458 475 V5.
FT CHAIN 525 879 GP41.
SQ SEQUENCE 879 AA; 99099 MW; BC6422ADDF1A3409 CRC64;

Query Match 89.0%; Score 113; DB 15; Length 879;
Best Local Similarity 81.8%; Pred. No. 4, 6e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVLYCTSVQWNET 22
DB 605 LLSWGCKGRVLYCTSVQWNET 626

RESULT 13
ID Q8Q7H1 PRELIMINARY; PRT; 880 AA.
AC Q8Q7H1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CMA407;
RX MEDLINE=21849375; PubMed=11860674;
RA Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kaput L.,
RA Ngansop C., Zekeng L., Gurtler L.G., Devare S.G., Brennan C.A.;
RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five

```

RT Phylogenetic Clusters:
RT AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL: A383250; AAL98872.1;
SQ SEQUENCE 880 AA; 99784 MW; F50D9358BED301EE CRC64;

Query Match
Best Local Similarity 89.0%; Score 113; DB 15; Length 880;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 LLSWGCKGRLVCTSVQNMET 22
DB 608 LLSWGCKGRLVCTSVQNMET 629

RESULT 14
ID Q807F9 PRELIMINARY; PRT; 882 AA.
AC Q807F9;
DT 01-JUN-2002 (TRENBLREL. 21, Created)
01-JUN-2002 (TRENBLREL. 21, Last sequence update)
01-JUN-2002 (TRENBLREL. 21, Last annotation update)
Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CMA100;
RX MEDLINE=21849375; PubMed=11860674;
RA Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kaput L.,
Nganop C., Zekeng L., Gurtler L.G., Devare S.G., Brennan C.A.;
RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
Phylogenetic Clusters."
RL AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL: AF383252; AAL98884.1;
SQ SEQUENCE 882 AA; 99439 MW; 627BCA5D0C09C6D4 CRC64;

Query Match
Best Local Similarity 89.0%; Score 113; DB 15; Length 882;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLSWGCKGRLVCTSVQNMET 22
DB 613 LLSWGCKGRLVCTSVQNMET 634

RESULT 15
ID Q807H6 PRELIMINARY; PRT; 887 AA.
AC Q807H6;
DT 01-JUN-2002 (TRENBLREL. 21, Created)
01-JUN-2002 (TRENBLREL. 21, Last sequence update)
01-JUN-2002 (TRENBLREL. 21, Last annotation update)
Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CMA124;
RX MEDLINE=21849375; PubMed=11860674;
RA Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kaput L.,
Nganop C., Zekeng L., Gurtler L.G., Devare S.G., Brennan C.A.;
RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
Phylogenetic Clusters."
RL AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL: AF383245; AAL98867.1;
SQ SEQUENCE 887 AA; 99366 MW; E210F1E3F7B2474D CRC64;

Query Match
Best Local Similarity 89.0%; Score 113; DB 15; Length 887;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLSWGCKGRLVCTSVQNMET 22
DB 618 LLSWGCKGRLVCTSVQNMET 639

Search completed: May 29, 2003, 10:39:15
Job time : 22.6984 secs

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Run on: May 29, 2003, 10:30:20 ; Search time 29.3333 Seconds

(without alignments)
99.938 Million cell updates/sec

Title: US-09-147-362A-4
Perfect score: 126
Sequence: 1 LLSWGCKGRLVCYTSVQWNST 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched: 908470 seqs, 133250620 residues
1 number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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17:	/SID2/gcgdata/genseq/genseqp-emb1/AA1996.DAT *
18:	/SID2/gcgdata/genseq/genseqp-emb1/AA1997.DAT *
19:	/SID2/gcgdata/genseq/genseqp-emb1/AA1998.DAT *
20:	/SID2/gcgdata/genseq/genseqp-emb1/AA1999.DAT *
21:	/SID2/gcgdata/genseq/genseqp-emb1/AA2000.DAT *
22:	/SID2/gcgdata/genseq/genseqp-emb1/AA2001.DAT *
23:	/SID2/gcgdata/genseq/genseqp-emb1/AA2002.DAT *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	126	100.0	22	19	AAW80462	Peptide derived from HIV-1 group O isolate
2	122	96.8	22	19	AAW80461	Peptide derived from HIV-1 group O isolate
3	122	96.8	22	19	AAW80463	Peptide derived from HIV-1 group O isolate
4	119	94.4	22	19	AAW80466	Peptide derived from HIV-1 group O isolate
5	115	91.3	40	17	AAW07346	Partial sequence of HIV-1 group O isolate
6	113	89.7	22	19	AAW80460	Peptide derived from HIV-1 group O isolate
7	113	89.7	40	17	AAW07352	Partial sequence of HIV-1 group O isolate
8	112	88.9	32	19	AAW80469	Peptide derived from HIV-1 group O isolate
9	112	88.9	41	17	AAW07351	Partial sequence of HIV-1 group O isolate
10	112	88.9	113	20	AAV05565	Partial sequence of HIV-1 group O isolate

11	112	88.9	715	20	AAV05625
12	111	88.1	21	AAAB1262	12
13	111	88.1	113	20	AAV05559
14	110	87.3	33	21	AAAB1231
15	110	87.3	40	17	AAAB0733
16	110	87.3	40	17	AAAB0734
17	110	87.3	41	17	AAAB0735
18	110	87.3	117	20	AAV05548
19	109	86.5	116	20	AAV05555
20	108	85.7	22	19	AAAB0464
21	108	85.7	22	19	AAAB0465
22	108	85.7	23	20	AAAB0563
23	108	85.7	33	21	AAAB1232
24	108	85.7	40	17	AAAB0734
25	108	85.7	113	20	AAV05551
26	108	85.7	113	20	AAV05550
27	108	85.7	129	21	AAAB69318
28	108	85.7	129	21	AAAB72828
29	108	85.7	150	19	AAAB69319
30	108	85.7	173	21	AAAB72829
31	108	85.7	200	19	AAV05551
32	108	85.7	200	23	AAAB22908
33	108	85.7	200	23	AAAB68319
34	108	85.7	215	20	AAV09449
35	108	85.7	215	20	AAV06983
36	108	85.7	215	21	AAV77374
37	108	85.7	215	21	AAV77374
38	108	85.7	245	20	AAV09443
39	108	85.7	245	21	AAV06977
40	108	85.7	281	20	AAV07369
41	108	85.7	373	20	AAV09507
42	108	85.7	373	20	AAV09495
43	108	85.7	460	20	AAV06979
44	108	85.7	460	20	AAV09500
45	108	85.7	460	20	AAV06984
			460	21	AAV77375

ALIGNMENTS

RESULT 1

ID AAW80462 standard; peptide; 22 AA.
 YX

AC AAW80462 ;

DT 28-JAN-1999 (first entry)
 VY

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

OS Immune deficiency virus.
OS synthetic.

PN W09845323-A1

PD 15-OCT-1998
yy

PF 06-APR-1998; 98WO-FR00691
XX

PR	09-APR-1997;	97FR-0004356
FR	24-FEB-1998;	98FR-0002212

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY
v

DR WPI; 1998-583190/49.
XX

PT human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.
 CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 126; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.2e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCTSVQMNST 22
 DB 1 LLSWGCKGRLVCTSVQMNST 22

JLT 2
 ID AAW80461 standard; peptide; 22 AA.

AAW80461;
 DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.

OS Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

XX (SNFI) PASTEUR SANOPI DIAGNOSTICS SA.

PA Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

PI WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 22 AA;

Query Match 96.8%; Score 122; DB 19; Length 22;
 Best Local Similarity 95.5%; Pred. No. 2.7e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCTSVQMNST 22
 DB 1 LLSWGCKGRLVCTSVQMNST 22

RESULT 3
 ID AAW80463
 XX AAW80463 standard; peptide; 22 AA.

AC AAW80463;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.

OS Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

XX (SNFI) PASTEUR SANOPI DIAGNOSTICS SA.

PA Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

PI WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 22 AA;

Query Match 96.8%; Score 122; DB 19; Length 22;
 Best Local Similarity 95.5%; Pred. No. 2.7e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCTSVQMNST 22
 DB 1 LLSWGCKGRLVCTSVQMNST 22

RESULT 4
 ID AAW80466
 XX AAW80466 standard; peptide; 22 AA.

AC AAW80466;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.

OS Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

XX 24-FEB-1998; 98FR-0002212.
 PR 09-APR-1997; 97FR-0004356.
 XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 XX Cheneboux DMB, Delagneau JFH, Gabelle SX, Rieunier FY;
 DR WPI; 1998-583190/49.
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 PS Claim 6; Page 43; 55pp; French.
 CC AAM80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 SQ Sequence 22 AA;
 Query Match 94.4%; Score 119; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 6.7e-09;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 LLSWGCKGRLVCTSVQNMST 22
 DB 1 LLSWGCKGRLVCTSVQNMST 22
 RESULT 5
 AAM07346
 ID AAM07346 standard; peptide; 40 AA.
 XX AAM07346;
 AC AAM07346;
 XX 03-JUN-1997 (first entry)
 DT 03-JUN-1997 (first entry)
 XX Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).
 XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
 KM C23V-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
 KM primer; hybridisation; amplification; PCR; polymerase chain reaction;
 KM immunogen; antibody.
 KM Human immunodeficiency virus type 1.
 PN MO9627013-A1.
 XX 06-SEP-1996.
 PD 06-SEP-1996.
 XX 26-FEB-1996; 96WO-FR00294.
 PF 26-FEB-1996; 96WO-FR00294.
 XX 27-FEB-1995; 95FR-0002236.
 PR 27-FEB-1995; 95FR-0002236.
 XX (ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 PA (INEM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX Chateix-Baudier ML, Louselet-Ajaka I, Ly T, Saragosti S, Simon F;
 PI WPI; 1996-412779/41.
 DR N-P8DB; AAT44922.
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 PT immunogens
 PS Claim 12; Page 34; 71pp; French.
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently

CC divided into 2 major groups based on the nucleotide sequences of the
 CC envelope gene (env): group M containing sub-groups A-G and group O
 CC containing the strains ANR70 and MYP5180. The invention relates to the
 CC discovery of several new strains of HIV-1 which can be placed in group O,
 CC based on the partial sequences of the C23V-env, gp41 and gag genes (see
 CC AAT44907-39 and AAM07339-64). The novel strains have been deposited as
 CC retroviruses CMCN I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07
 CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
 CC presented here is from the strain BCF07 (MAN) and corresponds to a
 CC fragment of the gp41 protein encoded by the env gene. The nucleic acids
 CC can be used to detect gp. O HIV-1 strains by hybridisation or (as
 CC primers) by gene amplification, also for screening and typing of such
 CC strains. Peptides encoded by the nucleic acids can be used as immunogens
 CC to raise Ab for detecting gp. O HIV-1.
 SQ Sequence 40 AA;
 Query Match 91.3%; Score 115; DB 17; Length 40;
 Best Local Similarity 86.4%; Pred. No. 3.9e-08;
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 1 LLSWGCKGRLVCTSVQNMST 22
 DB 19 LLSWGCKGRLVCTSVQNMST 40
 RESULT 6
 AAM80460
 ID AAM80460 standard; peptide; 22 AA.
 XX AAM80460;
 AC AAM80460;
 XX 28-JAN-1999 (first entry)
 DT 28-JAN-1999 (first entry)
 XX Peptide derived from a conserved sequence of group O human HIV.
 DE Peptide derived from a conserved sequence of group O human HIV.
 XX Group O human immune deficiency virus; HIV; detection; infection.
 KM Synthetic.
 XX Immune deficiency virus.
 XX MO9845323-A1.
 XX 15-OCT-1998.
 PD 15-OCT-1998.
 XX 06-APR-1998; 98WO-FR00691.
 PF 06-APR-1998; 98WO-FR00691.
 XX 24-FEB-1998; 98FR-0002212.
 PR 09-APR-1997; 97FR-0004356.
 XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 PA Cheneboux DMB, Delagneau JFH, Gabelle SX, Rieunier FY;
 PI WPI; 1998-583190/49.
 DR WPI; 1998-583190/49.
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 PS Claim 6; Page 42; 55pp; French.
 CC AAM80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 SQ Sequence 22 AA;
 Query Match 89.7%; Score 113; DB 19; Length 22;
 Best Local Similarity 86.4%; Pred. No. 4e-08;
 Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;


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XX 27-FEB-1995; 95FR-0002236.
XX
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Chaux-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F,
XX WPI; 1996-412779/41.
XX
XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
XX antibodies - useful for diagnosis, screening and typing, or as
XX immunogens
XX
XX Claim 12; Page 46; 71pp; French.
XX
XX Human immunodeficiency virus type 1 (HIV-1) strains are currently
XX divided into 2 major groups based on the nucleotide sequences of the
XX envelop gene (env): group M containing sub-groups A-G, and group O
XX containing the strains HTM70 and MYP5180. The invention relates to the
XX discovery of several new strains of HIV-1 which can be placed in group O,
XX based on the partial sequences of the C2V3-env, gp41 and gag genes (see,
XX CC AAT44907-39 and AAM07329-64). The novel strains have been deposited as
XX CC retroviruses CCMC I-1544 (BCP02 (ESS)), 1543 (BCP01 (FAN)), 1546 (BCP07
XX CC (MAN)), 1547 (BCP08 (NKO)) and 1545 (BCP03 (POC)). The sequence
XX presented here is from the strain BCF12 and corresponds to a fragment of
XX the gp41 protein encoded by the env gene. The nucleic acids can be used
XX to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene
XX amplification, also for screening and typing of such strains. Peptides
XX encoded by the nucleic acids can be used as immunogens to raise Ab for
XX detecting gp. O HIV-1.
XX
XX SQ Sequence 41 AA;
XX
XX Query Match 88.9%; Score 112; DB 17; Length 41;
XX Best Local Similarity 81.8%; Pred. No. 9.7e-08;
XX Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 LLSWGCKGRLVCTSVQNMNST 22
XX Db 19 LNLWGCKGRLVCTSVQNMNST 40
XX
XX RESULT 10
XX AAY05565
XX ID AAY05565 standard; Protein; 113 AA.
XX
XX AAY05565;
XX
XX 19-JUL-1999 (first entry)
XX
XX HIV-1 group O isolate MP539-PBMC gp41 antigen.
XX
XX HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
XX vaccine; diagnosis; AIDS.
XX
XX Human immunodeficiency virus type 1.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 65 /note= "encoded by AMW"
XX FT Misc-difference 74 /note= "encoded by ATR"
XX FT Misc-difference 84 /note= "encoded by GAK"
XX FT Misc-difference 86 /note= "encoded by AGY"
XX
XX WO9904011-A2.
XX
XX 28-JAN-1999.
XX
XX 20-JUL-1998; 98WO-EP04522.
XX
XX PF

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XX 18-JUL-1997; 97EP-0870110.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
XX WPI; 1999-132255/11.
XX
XX N-PSDB; AAY05565.
XX
XX New isolated HIV-1 group O strains - used to produce
XX polynucleotides, antigens and antibodies for use in diagnosis and in
XX vaccines for prevention of HIV-1 infection
XX
XX Claim 3; Fig 6; 162pp; English.
XX
XX The present sequence is an antigen of the gp41 protein of HIV-1
XX group O (Outlier) strain MP539-PBMC, a Cameroon isolate. The
XX invention relates to new HIV-1 group O antigens (see AAY05546-625),
XX and the use of these antigens, or nucleic acids encoding them (see
XX CC AAX25154-80), in the diagnosis and prophylaxis of AIDS. They can be
XX used as reagents for detecting HIV-1 group O infection and for
XX CC differentiating different types of HIV-1 group O infection.
XX Vaccines that provide protective immunity against HIV-1 infection, in
XX CC particular against HIV-1 group O infection, comprise at least one
XX CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a
XX CC virus-like particle comprising such an antigen, or an attenuated
XX CC form of an HIV-1 type O strain. The invention also relates to new
XX CC HIV-1 group O strains, mostly from patients from Cameroon and its
XX CC neighbouring countries.
XX
XX SQ Sequence 113 AA;
XX
XX Query Match 88.9%; Score 112; DB 20; Length 113;
XX Best Local Similarity 81.8%; Pred. No. 2.5e-07;
XX Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 LLSWGCKGRLVCTSVQNMNST 22
XX Db 39 LNLWGCKGRLVCTSVQNMNST 60
XX
XX RESULT 11
XX AAY05625
XX ID AAY05625 standard; Protein; 715 AA.
XX
XX AAY05625;
XX
XX 19-JUL-1999 (first entry)
XX
XX HIV-1 group O isolate MP645 envelope protein (Env).
XX
XX HIV-1 group O; Outlier strain; envelope protein; Env; antigen;
XX vaccine; diagnosis; AIDS.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO9904011-A2.
XX
XX 28-JAN-1999.
XX
XX 20-JUL-1998; 98WO-EP04522.
XX
XX 18-JUL-1997; 97EP-0870110.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
XX WPI; 1999-132255/11.
XX
XX N-PSDB; AAX25180.
XX
XX New isolated HIV-1 group O strains - used to produce
XX
XX PF

```

PT polynucleotides, antigens and antibodies for use in diagnosis and in
 PT vaccines for prevention of HIV-1 infection
 PS Claim 3; Fig 8A; 162pp; English.
 XX
 CC The present sequence is a partial Env polypeptide of HIV-1 group O
 CC (Outlier) virus isolate Mp645, as deduced from part of the genome
 CC of MP645 (see AAX25180). The invention relates to new HIV-1 group O
 CC antigens, especially envelope protein antigens (see AAY05546-625),
 CC and the use of these antigens, or nucleic acids encoding them (see
 CC AAX25154-80), in the diagnosis and prophylaxis of AIDS. They can be
 CC used as reagents for detecting HIV-1 group O infection and for
 CC differentiating different types of HIV-1 group O infection.
 CC Vaccines that provide protective immunity against HIV-1 infection,
 CC in particular against HIV-1 group O infection, comprise at least
 CC one HIV-1 type O antigen, a nucleic acid encoding such an antigen,
 CC a virus-like particle comprising such an antigen, or an attenuated
 CC form of an HIV-1 type O strain. The invention also relates to new
 CC HIV-1 group O strains, obtained from patients from Cameroon, Gabon,
 CC Tchad, Nigeria, Senegal and Niger.
 SQ Sequence 715 AA;
 Query Match 88.9%; Score 112; DB 20; Length 715;
 Best Local Similarity 86.4%; Pred. No. 1.4e-06;
 Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LLSWGCKGRVLCYTSVQMNST 22
 ||:|||||||
 DB 628 LLLNMGCKRGLVCTSVQMNRT 649
 RESULT 12
 ID AAB12212
 AA B12212 standard; peptide; 33 AA.
 AC AAB12212;
 DT 10-NOV-2000 (first entry)
 XX
 DE Partial sequence of HIV-1 strain BCF13 gp41 immunodominant region.
 XX
 KW HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
 XX acquired immunodeficiency syndrome; group O HIV; gp41; BCF13.
 OS Human immunodeficiency virus type 1.
 XX
 EP1013766-A2.
 28-JUN-2000.
 PF 29-NOV-1999; 99EP-0309491.
 XX
 PR 30-NOV-1998; 98US-0110292.
 PR 08-FEB-1999; 99US-0119138.
 PR 04-NOV-1999; 99US-0433428.
 XX
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 XX
 PI De Lays R, Zheng J;
 XX
 DR WPI; 2000-402205/35.
 XX
 PT New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PT virus group O antibodies -
 XX
 PS Example 1; Fig 1; 52pp; English.
 XX
 CC The present sequence is a partial gp41 protein of Human Immunodeficiency
 CC Virus Type 1 (HIV-1) strain BCF13. HIV is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of

CC antibodies produced in response to HIV infection. BCF13 is a member of
 CC HIV group O (outlier). The present sequence is the immunodominant region
 CC of gp41. This sequence was used in a sequence homology alignment,
 CC which in turn was used to derive a consensus sequence peptide: peptide
 CC 147 (AAB12254).
 XX
 SQ Sequence 33 AA;
 Query Match 88.1%; Score 111; DB 21; Length 33;
 Best Local Similarity 90.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLSWGCKGRVLCYTSVQMN 20
 ||:|||||||
 DB 14 LLSWGCKGRVLCYTSVQMN 33
 RESULT 13
 ID AAY05559
 AA Y05559 standard; protein; 113 AA.
 AC AAY05559;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE HIV-1 group O isolate BSD189 gp41 antigen.
 XX
 KW HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
 KW vaccine; diagnosis; AIDS.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9904011-A2.
 XX
 PD 28-JAN-1999.
 XX
 PE 20-JUL-1998; 98WO-EP04522.
 XX
 PR 18-JUL-1997; 97EP-0870110.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
 XX
 DR WPI; 1999-132255/11.
 DR N-PSDB; AAX25167.
 XX
 PT New isolated HIV-1 group O strains - used to produce
 PT polynucleotides, antigens and antibodies for use in diagnosis and in
 PT vaccines for prevention of HIV-1 infection
 XX
 PS Claim 3; Fig 6; 162pp; English.
 XX
 CC The present sequence is an antigen of the gp41 protein of HIV-1
 CC group O (Outlier) strain BSD189, a Cameroon isolate. The
 CC invention relates to new HIV-1 group O antigens (see AAY05546-625),
 CC and the use of these antigens, or nucleic acids encoding them (see
 CC AAX25154-80), in the diagnosis and prophylaxis of AIDS. They can be
 CC used as reagents for detecting HIV-1 group O infection and for
 CC differentiating different types of HIV-1 group O infection.
 CC Vaccines that provide protective immunity against HIV-1 infection,
 CC in particular against HIV-1 group O infection, comprise at least one
 CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a
 CC virus-like particle comprising such an antigen, or an attenuated
 CC form of an HIV-1 type O strain. The invention also relates to new
 CC HIV-1 group O strains, mostly from patients from Cameroon and its
 CC neighbouring countries.
 XX
 SQ Sequence 113 AA;
 Query Match 88.1%; Score 111; DB 20; Length 113;
 Best Local Similarity 81.8%; Pred. No. 3.3e-07;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRILVCYTSVQNMST 22
DB 39 LLSWGCKGRILVCYTSVQNMST 60

RESULT 14
ID AAB12231 standard; peptide; 33 AA.
AC AAB12231;
XX 10-NOV-2000 (first entry)
DT Partial sequence of HIV-1 strain MAN gp41 immunodominant region.
DE HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
XX acquired immunodeficiency syndrome; group O HIV; gp41; MAN.
KM Human immunodeficiency virus type 1.
XX EPI013766-A2.
PD 28-JUN-2000.
XX 29-NOV-1999; 99EP-0309491.
PF 30-NOV-1996; 98US-0110292.
PR 08-FEB-1999; 99US-0119138.
PR 04-NOV-1999; 99US-0433428.
XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
PI De Leye R, Zheng J;
FI WPI; 2000-402205/35.
DR New antigenic peptides and peptide functional derivatives, useful for
XX detection of antibodies produced in response to human immunodeficiency
PT virus group O antibodies -
XX Example 1; Fig 1; 52pp; English.
PS The present sequence is a partial gp41 protein of Human Immunodeficiency
CC Virus Type 1 (HIV-1) strain MAN. HIV is the principle aetiological
CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
CC envelope protein, and may be used as an antigen for the detection of
CC HIV group O (outlier). The present sequence is the immunodominant region
CC of gp41. This sequence was used in a sequence homology alignment,
CC which in turn was used to derive a consensus sequence peptide: peptide
CC 147 (AAB12254).
SQ Sequence 33 AA;
XX

Query Match 87.3%; Score 110; DB 21; Length 33;
Best Local Similarity 90.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLSWGCKGRILVCYTSVQNMST 20
DB 14 LLSWGCKGRILVCYTSVQNMST 33

RESULT 15
ID AAM07343 standard; peptide; 40 AA.
AC AAM07343;
XX 03-JUN-1997 (first entry)
DT Partial sequence of gp41 from HIV-1 gp. O strain BCF02 (ESS).
XX

XX Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;
KM C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
KM primer; hybridisation; amplification; PCR; polymerase chain reaction;
KM immunogen; antibody.
XX Human immunodeficiency virus type 1.
OS WO9627013-A1.
XX 06-SEP-1996.
PD 26-FEB-1996; 96MO-FR00294.
PF 27-FEB-1995; 95FR-0002236.
PR (ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;
PI WPI; 1996-412779/41.
DR N-PSDS; AAT44918.
XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
PT antibodies - useful for diagnosis, screening and typing, or as
PT immunogens
PS Claim 12; Page 33; 71pp; French.
XX Human immunodeficiency virus type 1 (HIV-1) strains are currently
CC divided into 2 major groups based on the nucleotide sequences of the
CC envelop gene (env): group M containing sub-groups A-O, and group O
CC containing the strains ANT70 and MYP5160. The invention relates to the
CC discovery of several new strains of HIV-1 which can be placed in group O,
CC based on the partial sequences of the C2V3-env, gp41 and gag genes (see
CC retroviruses CCM 1-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07
CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
CC presented here is from the strain BCF02 (ESS) and corresponds to a
CC fragment of the gp41 protein encoded by the env gene. The nucleic acids
CC can be used to detect gp. O HIV-1 strains by hybridisation or (as
CC primers) by gene amplification, also for screening and typing of such
CC strains. Peptides encoded by the nucleic acids can be used as immunogens
CC to raise Ab for detecting gp. O HIV-1.
SQ Sequence 40 AA;
XX

Query Match 87.3%; Score 110; DB 17; Length 40;
Best Local Similarity 81.8%; Pred. No. 1.7e-07;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 LLSWGCKGRILVCYTSVQNMST 22
DB 19 LLSWGCKGRILVCYTSVQNMST 40

Search completed: May 29, 2003, 10:36:21
Job time : 29.3333 secs

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MOLECULE TYPE: peptide
US-08-894-699-39

Query Match 91.3%; Score 115; DB 3; Length 40;
Best Local Similarity 86.4%; Pred. No. Se-10;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQWNST 22
||:|||||:|||||:
Db 19 LLSWGCKGRIVCYTSVQWNET 40

RESULT 2
US-09-444-410-39

Sequence 39, Application US/09444410
Patent No. 6270975

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SENTOB

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOI-DUONG

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

TITLE OF INVENTION: VIRUSES, AND USES THEREOF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

STREET: FLOOR

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/444,410

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/894,699

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-444-410-39

Query Match 91.3%; Score 115; DB 4; Length 40;

Best Local Similarity 86.4%; Pred. No. Se-10;

Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQWNST 22
||:|||||:|||||:
Db 19 LLSWGCKGRIVCYTSVQWNET 40

RESULT 3
US-08-894-699-68

Sequence 68, Application US/08894699
Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SENTOB

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOI-DUONG

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

TITLE OF INVENTION: VIRUSES, AND USES THEREOF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

STREET: FLOOR

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,699

FILING DATE: 01-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294

FILING DATE: 26-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-894-699-68

Query Match 89.7%; Score 113; DB 3; Length 40;

Best Local Similarity 86.4%; Pred. No. 9.7e-10;

Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQWNST 22
||:|||||:|||||:
Db 19 LLSWGCKGRIVCYTSVQWNET 40

RESULT 4
US-09-444-410-68

Sequence 68, Application US/09444410
Patent No. 6270975

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SENTOB

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-68

Query Match 89.7%; Score 113; DB 4; Length 40;
Best Local Similarity 86.4%; Pred. No. 9.7e-10;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTSVQMNST 22
19 LLSWGCKGRIVCYTSVQMNST 40

RESULT 5
US-08-894-699-67
Sequence 67, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEST-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-67

Query Match 88.9%; Score 112; DB 3; Length 41;
Best Local Similarity 81.8%; Pred. No. 1.4e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTSVQMNST 22
Db 19 LLSWGCKGRIVCYTSVQMNST 40

RESULT 6
US-09-444-410-67
Sequence 67, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEST-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
09-444-410-67

Query Match
Best Local Similarity 88.9%; Score 112; DB 4; Length 41;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQWNST 22
Db 19 LLSWGCKGRIVCYTSVQWNST 40

RESULT 7
US-09-433-428D-6
Sequence 6, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leyer, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 33
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
09-433-428D-6

Query Match
Best Local Similarity 90.0%; Score 111; DB 4; Length 33;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQWN 20
Db 14 LLSWGCKGRIVCYTSVQWN 33

RESULT 8
US-09-433-428D-25
Sequence 25, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leyer, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 33

TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-25

Query Match
Best Local Similarity 87.3%; Score 110; DB 4; Length 33;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQWN 20
Db 14 LLSWGCKGRIVCYTSVQWN 33

RESULT 9
US-08-894-699-36
Sequence 36, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEY-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-36

Query Match
Best Local Similarity 87.3%; Score 110; DB 3; Length 40;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQWNST 22
Db 19 LLSWGCKGRIVCYTSVQWNST 40

RESULT 10
US-08-894-699-37
; Sequence 37, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-37

Query Match 87.3%; Score 110; DB 3; Length 40;
; Best Local Similarity 81.8%; Pred. No. 2.6e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 19 LLSWGCKGRILCYTSVQNMST 40

RESULT 11
US-09-444-410-36
; Sequence 36, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,410
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,699
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-444-410-36

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,410
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,699
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-444-410-36

Query Match 87.3%; Score 110; DB 4; Length 40;
; Best Local Similarity 81.8%; Pred. No. 2.6e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 19 LLSWGCKGRILCYTSVQNMST 40

RESULT 12
US-09-444-410-37
; Sequence 37, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA

COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-37

Query Match 87.3%; Score 110; DB 4; Length 40;
Best Local Similarity 81.8%; Pred. No. 2.6e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRVCTSVQNMNST 22
DB 19 LLSWGCKGRVCTSVQNMNST 40

RESULT 13
US-08-894-699-69
Sequence 69, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-69

Query Match 87.3%; Score 110; DB 3; Length 41;
Best Local Similarity 81.8%; Pred. No. 2.7e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRVCTSVQNMNST 22
DB 19 LLSWGCKGRVCTSVQNMNST 40

RESULT 14
US-09-444-410-69
Sequence 69, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 69:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 41 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-444-410-69

Query Match 87.3%; Score 110; DB 4; Length 41;
 Best Local Similarity 81.8%; Pred. No. 2.7e-09;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTSVQNMST 22
 ||:|||||:|||||:|
 Db 19 LLSWGCKGRIVCYTSVQNMNT 40

; LT 15
 ; US-09-433-428D-30
 ; Sequence 30, Application US/09433428D
 ; Patent No. 6149910
 ; GENERAL INFORMATION:
 ; APPLICANT: De Leys, Robert J.
 ; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
 ; FILE REFERENCE: CDS-207
 ; CURRENT APPLICATION NUMBER: US/09/433,428D
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 30
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 ; US-09-433-428D-30

Query Match 85.7%; Score 108; DB 4; Length 33;
 Best Local Similarity 85.0%; Pred. No. 4.2e-09;
 Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTSVQNM 20
 ||:|||||:|||||:|
 Db 14 LLSWGCKGRIVCYTSVKMN 33

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 time : 9.95238 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:39:21 ; Search time 19.0317 Seconds

(without alignments)
117.011 Million cell updates/sec

Title: US-09-147-362a-4

Perfect score: 126

Sequence: 1 LLSWGCKGRLVCTYSVQMNST 22

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Searched: 383519 segs, 101223694 residues

1 number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pcp.*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*

9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*

11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*

12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pcp.*

13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*

14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108	85.7	37	9	US-10-026-741-86
2	108	85.7	200	10	US-08-854-816-104
3	108	85.7	215	1	US-08-911-824-58
4	108	85.7	245	1	US-08-911-824-48
5	108	85.7	281	1	US-08-911-824-120
6	108	85.7	373	1	US-08-911-824-52
7	108	85.7	460	1	US-08-911-824-60
8	108	85.7	488	1	US-08-911-824-95
9	108	85.7	490	1	US-08-911-824-95
10	108	85.7	526	1	US-08-911-824-97
11	108	85.7	618	1	US-08-911-824-97
12	108	85.7	706	1	US-08-911-824-93
13	108	85.7	736	1	US-08-911-824-91
14	108	85.7	873	1	US-08-911-824-61
15	102	81.0	35	9	US-10-026-741-101
16	102	81.0	37	9	US-10-026-741-7
17	102	81.0	37	9	US-10-026-741-90
18	102	81.0	351	9	US-10-026-741-47
19	102	81.0	877	9	US-10-026-741-102

20	101	80.2	37	9	US-10-026-741-94	Sequence 94, App1
21	101	80.2	104	9	US-10-026-741-100	Sequence 100, App
22	100	79.4	37	9	US-10-026-741-88	Sequence 88, App1
23	100	79.4	213	10	US-09-854-816-103	Sequence 103, App
24	98	77.8	35	9	US-09-886-156-62	Sequence 62, App1
25	98	77.8	35	9	US-09-886-150-62	Sequence 62, App1
26	98	77.8	35	9	US-09-886-149-62	Sequence 62, App1
27	98	77.8	35	9	US-09-886-159-62	Sequence 62, App1
28	98	77.8	146	12	US-10-000-321-10	Sequence 10, App1
29	98	77.8	204	10	US-09-854-816-105	Sequence 105, App
30	98	77.8	351	9	US-09-886-156-66	Sequence 46, App1
31	98	77.8	351	9	US-09-886-150-46	Sequence 46, App1
32	98	77.8	351	9	US-09-886-149-46	Sequence 46, App1
33	98	77.8	351	9	US-09-886-159-46	Sequence 46, App1
34	97	77.0	23	9	US-10-026-741-30	Sequence 30, App1
35	96	76.2	23	9	US-09-388-847-4	Sequence 4, App1
36	96	76.2	23	12	US-10-000-321-2	Sequence 2, App1
37	96	76.2	24	9	US-10-026-741-34	Sequence 34, App1
38	86	68.3	198	10	US-09-854-816-81	Sequence 81, App1
39	85	67.5	37	9	US-10-026-741-82	Sequence 82, App1
40	85	67.5	37	9	US-10-026-741-84	Sequence 84, App1
41	85	67.5	198	10	US-09-854-816-77	Sequence 77, App1
42	85	67.5	198	10	US-09-854-816-78	Sequence 78, App1
43	85	67.5	198	10	US-09-854-816-80	Sequence 80, App1
44	85	67.5	198	10	US-09-854-816-89	Sequence 89, App1
45	85	67.5	204	10	US-09-854-816-106	Sequence 106, App

ALIGNMENTS

RESULT 1
US-10-026-741-86
Sequence 86, Application US/10026741
Publication No. US20030049604A1

GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CIAVEL, FRANCOISE
BORMAN, ANDREW
QUILLIENT, CAROLINE
GUETARD, DENISE
MONTIGNIER, LUC
DONON DE SAINT-MARTIN, JACQUELINE
COHEN, JACQUES

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

```

NAME: Meyers, Kenneth J
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260, 6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-026-741-86

Query Match      85.7% Score 108; DB 9; Length 37;
Best Local Similarity 81.8% Pred. No. 1,2e-08;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 LLSWGCKGRALVCTYSVMNST 22
||| ||||| ||||| ||||| |||
14 LLSWGCKGKGLVCTYSVMNRT 35

RESULT 2
US-09-854-816-104
; Sequence 104, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Pheasant
Melissa A. Starovaanik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-854-816-104

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Query Match      85.7%; Score 108; DB 10; Length 200;
Best Local Similarity 81.8%; Pred. No. 5,9e-08;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1  LLSWGCKGRLVCYTSVQWNST 22
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Db      126  LLSIMGCKGRLVCYTSVKNMRT 147

RESULT 3
US-08-911-824-58
; Sequence 58, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165-US-01
; CURRENT APPLICATION NUMBER: US/08/911.824
; CURRENT FILING DATE: 1997-08-15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-8pL
US-08-911-824-58

Query Match      85.7%; Score 108; DB 1; Length 215;
Best Local Similarity 77.3%; Pred. No. 6.3e-08;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1  LLSWGCKGRLVCYTSVQWNST 22
      ||| |||||:|||||:|||||
Db      127  LLSIMGCKGRLVCYTSVKNMRT 148

RESULT 4
US-08-911-824-48
; Sequence 48, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165-US-01
; CURRENT APPLICATION NUMBER: US/08/911.824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-9pL
US-08-911-824-48

Query Match      85.7%; Score 108; DB 1; Length 245;

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Best Local Similarity 77.3%; Pred. No. 7.1e-08;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 LLSWGCKGRILCYTSVQWNST 22
||:|||||:|||||:|||||:
Db 127 LLNLWGCKGRILCYTSVKMNET 148

RESULT 5
US-08-911-824-120
; Sequence 120, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-15PL
US-08-911-824-120

Query Match 85.7%; Score 108; DB 1; Length 281;
Best Local Similarity 77.3%; Pred. No. 8.1e-08;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 LLSWGCKGRILCYTSVQWNST 22
||:|||||:|||||:|||||:
Db 127 LLNLWGCKGRILCYTSVKMNET 148

RESULT 6
US-08-911-824-52
; Sequence 52, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-11PL
US-08-911-824-52

Query Match 85.7%; Score 108; DB 1; Length 373;
Best Local Similarity 77.3%; Pred. No. 1.1e-07;

Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 LLSWGCKGRILCYTSVQWNST 22
||:|||||:|||||:|||||:
Db 127 LLNLWGCKGRILCYTSVKMNET 148

RESULT 7
US-08-911-824-60
; Sequence 60, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-8CKS
US-08-911-824-60

Query Match 85.7%; Score 108; DB 1; Length 460;
Best Local Similarity 77.3%; Pred. No. 1.3e-07;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 LLSWGCKGRILCYTSVQWNST 22
||:|||||:|||||:|||||:
Db 372 LLNLWGCKGRILCYTSVKMNET 393

RESULT 8
US-08-911-824-95
; Sequence 95, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-14PL
US-08-911-824-95

Query Match 85.7%; Score 108; DB 1; Length 488;
Best Local Similarity 77.3%; Pred. No. 1.4e-07;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTSVQNMST 22
||:|||||:|||||:|||||
Db 127 LNLWGCKGRILICTSVKMNET 148

RESULT 9
US-08-911-824-50
; Sequence 50, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-9CKS
US-08-911-824-50

Query Match 85.7%; Score 108; DB 1; Length 490;
Best Local Similarity 77.3%; Pred. No. 1.4e-07;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LLSWGCKGRIVCTSVQNMST 22
||:|||||:|||||:|||||
Db 372 LNLWGCKGRILICTSVKMNET 393

RESULT 10
US-08-911-824-97
; Sequence 97, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-15CKS
US-08-911-824-97

Query Match 85.7%; Score 108; DB 1; Length 526;
Best Local Similarity 77.3%; Pred. No. 1.5e-07;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTSVQNMST 22
||:|||||:|||||:|||||
Db 372 LNLWGCKGRILICTSVKMNET 393

RESULT 11
US-08-911-824-54
; Sequence 54, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-11CKS
US-08-911-824-54

Query Match 85.7%; Score 108; DB 1; Length 618;
Best Local Similarity 77.3%; Pred. No. 1.7e-07;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LLSWGCKGRIVCTSVQNMST 22
||:|||||:|||||:|||||
Db 372 LNLWGCKGRILICTSVKMNET 393

RESULT 12
US-08-911-824-93
; Sequence 93, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-13CKS
US-08-911-824-93

Query Match 85.7%; Score 108; DB 1; Length 706;
Best Local Similarity 77.3%; Pred. No. 1.9e-07;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LLSWGCKGRIVCTSVQNMST 22

Db 618 LNLNMGCKGRLLCYTSVKMNET 639

RESULT 13
US-08-911-824-91
Sequence 91, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165-US-01
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 91
LENGTH: 736
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-12CKS
US-08-911-824-91

Query Match 85.7%; Score 108; DB 1; Length 736;
Best Local Similarity 77.3%; Pred. No. 2e-07;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Cy 1 LLSWGCKGRLLCYTSVKMNET 22
Db 618 LNLNMGCKGRLLCYTSVKMNET 639

RESULT 14
US-08-911-824-61
Sequence 61, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165-US-01
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 61
LENGTH: 873
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: HIV-1 Group O isolate HAM112
US-08-911-824-61

Query Match 85.7%; Score 108; DB 1; Length 873;
Best Local Similarity 77.3%; Pred. No. 2.3e-07;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Cy 1 LLSWGCKGRLLCYTSVKMNET 22
Db 618 LNLNMGCKGRLLCYTSVKMNET 639

Db 601 LNLNMGCKGRLLCYTSVKMNET 622

RESULT 15
US-10-026-741-101
Sequence 101, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNÉAU, PIERRE
APPLICANT: CLAVEL, FRANÇOISE
APPLICANT: BORMAN, ANDREW
APPLICANT: OUILLET, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: MONTAGNER, LUC
APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE
APPLICANT: COHEN, JAOUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flanagan, Henderson, Farbow, Garrett &
Dunney, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026.741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-026-741-101

Query Match 81.0%; Score 102; DB 9; Length 35;
Best Local Similarity 72.7%; Pred. No. 8.1e-08;
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Cy 1 LLSWGCKGRLLCYTSVKMNET 22
Db 618 LNLNMGCKGRLLCYTSVKMNET 639

Search completed: May 29, 2003, 11:03:57
Job time : 20.0317 secs

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OM protein - protein search, using SW model

Run on: May 29, 2003, 10:33:06 ; Search time 10.8254 seconds
(without alignments)
195.370 Million cell updates/sec

Title: US-09-147-362a-4

Perfect score: 126

Sequence: 1 LLSWGCKGRLVCTYSVQNMST 22

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108	85.7	863	2 A53034	gag polyprotein -
2	102	81.0	877	2 S49197	envelope protein p
3	101	80.2	104	2 S52930	GP41 ENV protein -
4	85	67.5	357	2 S21990	envelope protein g
5	85	67.5	358	2 S22002	envelope protein g
6	85	67.5	443	2 C41621	env polyprotein p
7	85	67.5	853	2 S54384	envelope polyprote
8	85	67.5	854	1 VCLJST	env polyprotein pr
9	85	67.5	855	1 VCLJZR	env polyprotein pr
10	84	66.7	358	2 S22000	envelope protein g
11	84	66.7	358	2 S70417	envelope protein g
12	82	65.1	357	2 S22006	envelope protein g
13	82	65.1	357	2 S21994	envelope protein g
14	82	65.1	357	2 S22004	envelope protein g
15	82	65.1	357	2 S21996	envelope protein g
16	82	65.1	357	2 S21992	envelope protein g
17	82	65.1	358	2 S21998	envelope protein g
18	82	65.1	445	2 A41621	env polyprotein p
19	82	65.1	454	2 B41621	env polyprotein M
20	82	65.1	843	2 H44001	env polyprotein D
21	82	65.1	847	2 T09448	env polyprotein pr
22	82	65.1	847	2 S13289	envelope glycoprot
23	82	65.1	852	1 VCLJBR	env protein - huma
24	82	65.1	852	2 T12016	env polyprotein -
25	82	65.1	854	2 S13288	envelope glycoprot
26	82	65.1	855	2 VCLJAJ	env protein - huma
27	82	65.1	856	1 VCLJH3	env polyprotein pr
28	82	65.1	856	1 VCLJVL	env polyprotein pr
29	82	65.1	856	1 VCLJW	env polyprotein pr

30	82	65.1	856	1 A44963	env polyprotein pr
31	82	65.1	859	1 VCLJMN	env polyprotein pr
32	82	65.1	861	1 VCLJIV	env polyprotein pr
33	82	65.1	861	1 VCLJSC	env polyprotein pr
34	82	65.1	868	1 VCLJH4	env polyprotein pr
35	81	64.3	846	1 VCLJND	env polyprotein pr
36	80	63.5	786	2 S28084	env polyprotein -
37	76.5	60.7	151	2 S30448	env protein - huma
38	76.5	60.7	151	2 S30453	env protein - huma
39	76.5	60.7	151	2 S30452	env protein - huma
40	76.5	60.7	151	2 S30450	env protein - huma
41	76.5	60.7	151	2 S30451	env protein - huma
42	76	60.3	729	1 VCLJRX	env polyprotein pr
43	76	60.3	859	2 T01672	envelope polyprote
44	76	60.3	861	1 VCLJKB	env polyprotein pr
45	75	59.5	851	2 S33985	env polyprotein -

ALIGNMENTS

RESULT 1

A53034 gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999

C:Accession: A53034

R:Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborcht, B.; van der Groen, J. Virol. 68, 1586-1596, 1994

A:Title: Genomic cloning and complete sequence analysis of a highly divergent African hu

A:Reference number: A53034; MUID:94149849; PMID:8107220

A:Accession: A53034

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-863 <VAN>

A:Cross-references: GB:L02367

C:Superfamily: type B retrovirus env polyprotein

C:Keywords: polyprotein

Query Match 85.7%; Score 108; DB 2; Length 863;
Best Local Similarity 81.8%; Pred. No. 1.2e-07;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCTYSVQNMST 22
DB 594 LLSWGCKGRLVCTYSVQNMRT 615
|||||:|||||:|||||

RESULT 2

S49197 envelope protein precursor - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999

C:Accession: S49197

R:Charneau, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chameret, S.; Cohen, J.; Remy, submitted to the EMBL Data Library, July 1994

A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi

A:Reference number: S49197

A:Accession: S49197

A:Molecule type: DNA

A:Residues: 1-877 <CHA>

A:Cross-references: EMBL:X80020; NID:9510516; PIDN:CAA56323.1; PID:9510517

A:Experimental source: isolate VAV

C:Superfamily: type B retrovirus env polyprotein

C:Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein

F:1-30/domain: signal sequence #status predicted <SIG>

F:31-535/Product: coat protein gp120 #status predicted <CP1>

F:536-877/Product: coat protein gp41 #status predicted <CP2>

F:598-716/domain: transmembrane #status predicted <TMN>

F:59,88,139,148,159,184,188,198,230,242,263,270,277,292,302,333,345,357,367,396,404,

Query Match 81.0%; Score 102; DB 2; Length 877;
Best Local Similarity 72.7%; Pred. No. 8.6e-07;

Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQMNST 22
|||:|||||:|||||:|||||:
Db 607 LLLMGCKRRLICTTAVPMNKS 628

RESULT 3

GP41 ENV protein - human immunodeficiency virus type 1 (fragment)
S52930
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C:Accession: S52930
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, January 1995
A:Description: A novel HIV-1 O strain illustrates the diversity of the O group.
A:Reference number: S52929
A:Accession: S52930
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-104 <CON>
A:Cross-references: EMBL:X84328; NID:9695526; PIDN:CAA59066.1; PID:9695527
C:Superfamily: type E retrovirus env polyprotein

Query Match 80.2%; Score 101; DB 2; Length 104;
Best Local Similarity 68.2%; Pred. No. 1.9e-07;
Matches 15; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQMNST 22
|||:|||||:|||||:|||||:
Db 45 LLLMGCKRRLICTTAVPMNKS 66

RESULT 4

envelope protein gp120/gp41 - human immunodeficiency virus type 1
S21990
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 20
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21990; S70423
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by sequence analysis.
A:Reference number: S21990
A:Accession: S21990
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
submitted to the EMBL Data Library, July 1991
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332, 'X', 334-357 <STE2>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
C:Superfamily: type E retrovirus env polyprotein

Query Match 67.5%; Score 85; DB 2; Length 357;
Best Local Similarity 59.1%; Pred. No. 0.00011;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQMNST 22
|||:|||||:|||||:|||||:
Db 93 LLLMGCKRRLICTTAVPMNKS 114

RESULT 5

S52002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 3L

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S22002; S70418
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by sequence analysis.
A:Reference number: S21990
A:Accession: S22002
A:Molecule type: DNA
A:Residues: 1-358 <STE1>
A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
submitted to the EMBL Data Library, July 1991
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333, 'X', 335-358 <STE2>
A:Cross-references: EMBL:X61352; NID:960186
C:Superfamily: type E retrovirus env polyprotein

Query Match 67.5%; Score 85; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00011;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQMNST 22
|||:|||||:|||||:|||||:
Db 94 LLLMGCKRRLICTTAVPMNKS 115

RESULT 6

env polyprotein P - human immunodeficiency virus type 1 (fragment)
C41621
N:Alternate names: coat polyprotein
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gull, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1765038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BDP>
A:Cross-references: GB:M72230; NID:9328631; PIDN:AB03792.1; PID:9555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics: env

C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/DNA: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 67.5%; Score 85; DB 2; Length 443;
Best Local Similarity 59.1%; Pred. No. 0.00013;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQMNST 22
|||:|||||:|||||:|||||:
Db 332 LLLMGCKRRLICTTAVPMNKS 353

RESULT 7

S54384
envelope polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C:Accession: S54384
R:Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <THE>
A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385
A:Superfamily: type E retrovirus env polypotein
C:Keywords: polypotein

Query Match 67.5%; Score 85; DB 2; Length 853;
Best Local Similarity 59.1%; Pred. No. 0.00023;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 589 LLGIWCGSGKILCTTVPMNNS 610

RESULT 8

A:polypotein precursor - simian immunodeficiency virus SIVcpz
N:Alternate names: coat polypotein
C:Contains: coat protein gp120; coat protein gp41
C:Species: simian immunodeficiency virus SIVcpz

A>Note: host Pan troglodytes (chimpanzee)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S09990
R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990

A>Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Reference number: S09983; MUID:90259077; PMID:2188136
A:Accession: S09990
A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 1-854 <HUS>
A:Molecule type: DNA
A:Cross-references: EMBL:X52154; NID:G558866; PIDN:CAA36407.1; PID:G558874

C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-500/Product: coat protein gp120 #status predicted <CP1>
F:501-854/Product: coat protein gp41 #status predicted <CP2>

F:501-517/Domain: transmembrane #status predicted <TM1>
F:675-693/Domain: transmembrane #status predicted <TM2>
F:805-821/Domain: transmembrane #status predicted <TM3>
F:134,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 67.5%; Score 85; DB 1; Length 854;
Best Local Similarity 54.5%; Pred. No. 0.00023;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 582 LLGIWCGSGKAVCTTVPMNNS 603

RESULT 9

A:env polypotein precursor - human immunodeficiency virus Zr-6
N:Alternate names: coat polypotein

C:Species: human immunodeficiency virus Zr-6
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C:Accession: D26192
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Ch

Gene 52, 71-82, 1987
A>Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti
A:Reference number: A26192; MUID:87248097; PMID:3036660
A:Accession: D26192
A:Molecule type: DNA
A:Residues: 1-855 <SRI>

A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403

C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polypotein #status predicted <MPT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TM4>
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 67.5%; Score 85; DB 1; Length 855;
Best Local Similarity 59.1%; Pred. No. 0.00023;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 591 LLGIWCGSGKILCTTVPMNNS 612

RESULT 10

A:envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C:Accession: S22000

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL data library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi

A:Reference number: S21990
A:Accession: S22000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polypotein

Query Match 66.7%; Score 84; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00015;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 94 LLGIWCGSGKILCTTVPMNNS 115

RESULT 11
A:envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S70417
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:11736940
A:Accession: S70417

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STB>
A:Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185

C:Superfamily: type E retrovirus env polypotein
Query Match 66.7%; Score 84; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00015;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 94 LLGIWCGSGKILCTTVPMNNS 115

RESULT 12

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:31:50 ; Search time 5.4127 Seconds

(without alignments)
168.581 Million cell updates/sec

Title: US-09-147-362a-4

Perfect score: 126

Sequence: 1 L15SWGCKGRVCTTSVQMNST 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	67.5	853	ENV_HV122	P12487 human immun
2	85	67.5	854	ENV_STV2C	P12481 chimpanzee
3	85	67.5	855	ENV_HV126	P04580 human immun
4	82	65.1	843	ENV_HV122	P35961 human immun
5	82	65.1	847	ENV_HV121	P19550 human immun
6	82	65.1	847	ENV_HV122	P05880 human immun
7	82	65.1	851	ENV_HV128	P04582 human immun
8	82	65.1	852	ENV_HV128	P12488 human immun
9	82	65.1	852	ENV_HV128	P12488 human immun
10	82	65.1	853	ENV_HV128	P12488 human immun
11	82	65.1	853	ENV_HV128	P12488 human immun
12	82	65.1	855	ENV_HV128	P12488 human immun
13	82	65.1	855	ENV_HV128	P12488 human immun
14	82	65.1	856	ENV_HV128	P12488 human immun
15	82	65.1	856	ENV_HV128	P12488 human immun
16	82	65.1	856	ENV_HV128	P12488 human immun
17	82	65.1	856	ENV_HV128	P12488 human immun
18	82	65.1	856	ENV_HV128	P12488 human immun
19	82	65.1	856	ENV_HV128	P12488 human immun
20	82	65.1	856	ENV_HV128	P12488 human immun
21	82	65.1	856	ENV_HV128	P12488 human immun
22	82	65.1	856	ENV_HV128	P12488 human immun
23	82	65.1	856	ENV_HV128	P12488 human immun
24	82	65.1	856	ENV_HV128	P12488 human immun
25	82	65.1	856	ENV_HV128	P12488 human immun
26	82	65.1	856	ENV_HV128	P12488 human immun
27	82	65.1	856	ENV_HV128	P12488 human immun
28	82	65.1	856	ENV_HV128	P12488 human immun
29	82	65.1	856	ENV_HV128	P12488 human immun
30	82	65.1	856	ENV_HV128	P12488 human immun
31	82	65.1	856	ENV_HV128	P12488 human immun
32	82	65.1	856	ENV_HV128	P12488 human immun
33	82	65.1	856	ENV_HV128	P12488 human immun

34	72.5	57.5	856	1	ENV_HV2NZ	P05883 human immun
35	70	55.6	865	1	ENV_STVAT	P05886 simian immu
36	69.5	55.2	712	1	ENV_HV2S2	P32536 human immun
37	69.5	55.2	846	1	ENV_HV2SB	P12449 human immun
38	69.5	55.2	859	1	ENV_HV2D2	P15831 human immun
39	69.5	55.2	859	1	ENV_HV2ST	P20872 human immun
40	69.5	55.2	885	1	ENV_STV54	P12492 simian immu
41	69	54.8	851	1	ENV_HV2D1	P17755 human immun
42	69	54.8	851	1	ENV_HV2G1	P18040 human immun
43	69	54.8	858	1	ENV_HV2RO	P04577 human immun
44	69	54.8	859	1	ENV_HV2CA	P24105 human immun
45	69	54.8	860	1	ENV_HV2BE	P18094 human immun

ALIGNMENTS

RESULT 1	ENV_HV122	STANDARD	PRT	853 AA.
ID	ENV_HV122			
AC	P12487			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, last annotation update)			
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).			
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11683;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Theodore T., Buckler-White A.,			
RL	Submitted (NOV-1988) to the HIV data bank.			
CC	-----			
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CC	-----			
DR	EMBL; M22639; AAA45370.1; -			
DR	HIV; M22639; ENV45226.			
DR	InterPro: IPR000328; Env GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KW	Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	31	BY SIMILARITY.
FT	CHAIN	509	853	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	154	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	330	BY SIMILARITY.
FT	DISULFID	376	442	BY SIMILARITY.
FT	DISULFID	383	415	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	137	137	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	144	144	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	153	153	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	185	185	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	188	188	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	225	235	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .)

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FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 853 AA; 97043 MW; 849B08CBADF7008 CRC64;

Query Match 67.5%; Score 85; DB 1; Length 853;
Best Local Similarity 59.1%; Pred. No. 2.1e-05;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

```
Oy 1 LLSWMGCKGRVLCYTSVQNMST 22
Db 589 ILGIWCGSGKILCTTVPNNSS 610
```

```
RESULT 2
ENV_SIVCZ STANDARD; PRT; 854 AA.
```

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ID ENV_SIVCZ STANDARD; PRT; 854 AA.
AC P17281;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RX SEQUENCE FROM N.A.
MEDLINE=90259077; Pubmed=2188136;
Huet T., Chevalier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
-1- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPEPTIDE.
-----
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-----
CC EMBL: X52154; CAA36407.1; -.
CC PIR: S09990; VCLJST.
CC HIV: X52154; ENVSCPZ.
CC InterPro: IPR000328; Env_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC AIMS: PF00517; GP41; 1.
CC AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane.
CC Signal.
FT SIGNAL 1 30
FT CHAIN 31 500 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 501 854 TRANSMEMBRANE GLYCOPROTEIN.
FT TRANSMEM 501 517 POTENTIAL.
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FT TRANSMEM 675 693 POTENTIAL.
FT TRANSMEM 805 821 POTENTIAL.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 854 AA; 95803 MW; 2E249AFAD4F2D9B3 CRC64;
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Query Match 67.5%; Score 85; DB 1; Length 854;
Best Local Similarity 54.5%; Pred. No. 2.1e-05;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```

```
Oy 1 LLSWMGCKGRVLCYTSVQNMST 22
Db 582 ILGIWCGSGKAVCTTVPNNSS 603
```

```
RESULT 3
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126 STANDARD; PRT; 855 AA.
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RX SEQUENCE FROM N.A.
MEDLINE=87248097; Pubmed=3036660;
Stiniyasan A., Anand R., York D., Ranganathan P., Feorino P.,
Schoeneman G., Curran J., Kalyanaram V.S., Luciw P.A.,
Sanchez-Pescador R.;
"Molecular characterization of human immunodeficiency virus from
Zaire: nucleotide sequence analysis identifies conserved and variable
domains in the envelope gene.";
Gene 52:71-82(1987).
-----
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-----
CC EMBL: K03458; AAA45380.1; -.
CC PIR: D26192; VCLJZR.
```

DR HIV; K03458; ENV526.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP120, 1.
DR Pfam; PF00517; GP41, 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 510
FT CHAIN 511 855
FT DISULFID 53 73
FT DISULFID 118 207
FT DISULFID 125 198
FT DISULFID 130 155
FT DISULFID 220 249
FT DISULFID 230 241
FT DISULFID 298 332
FT DISULFID 378 444
FT DISULFID 385 417
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 145 145
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 186 186
FT CARBOHYD 189 189
FT CARBOHYD 199 199
FT CARBOHYD 236 236
FT CARBOHYD 243 243
FT CARBOHYD 264 264
FT CARBOHYD 278 278
FT CARBOHYD 291 291
FT CARBOHYD 297 297
FT CARBOHYD 333 333
FT CARBOHYD 340 340
FT CARBOHYD 355 355
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 398 398
FT CARBOHYD 404 404
FT CARBOHYD 443 443
FT CARBOHYD 447 447
FT CARBOHYD 460 460
FT CARBOHYD 461 461
FT CARBOHYD 464 464
FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 673 673
FT SEQUENCE 855 AA; 96971 MW; 384D3D6E239C3457 CRC64;
SQ
Query Match 67.5%; Score 85; DB 1; Length 855;
Best Local Similarity 59.1%; Pred. No. 2.1e-05;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 1 LLSWGCKGRVLCYTSVQMNST 22
Db 591 LLSWGCKGRVLCYTSVQMNST 612
RESULT 4
ENV_HV1Y2 STANDARD; PRT; 843 AA.
ID ENV_HV1Y2
AC P35561;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).

OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.O., Price R.W., Sharp P.M., Hahn B.H.,
Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
properties of human immunodeficiency virus type 1 in vivo: evidence
for limited defectiveness and complementation.";
RU J. Virol. 66:6587-6600(1992).
CC -----
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CC -----
CC EMBL; M93258; NOT ANNOTATED_CDS.
DR PIR; H44001; H44001.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP120, 1.
DR Pfam; PF00517; GP41, 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 489
FT CHAIN 490 843
FT TRANSMEM 738 755
FT DISULFID 53 73
FT DISULFID 118 201
FT DISULFID 125 192
FT DISULFID 130 155
FT DISULFID 214 243
FT DISULFID 224 235
FT DISULFID 292 326
FT DISULFID 373 432
FT DISULFID 380 405
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 138 138
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 193 193
FT CARBOHYD 230 230
FT CARBOHYD 237 237
FT CARBOHYD 258 258
FT CARBOHYD 272 272
FT CARBOHYD 285 285
FT CARBOHYD 291 291
FT CARBOHYD 297 297
FT CARBOHYD 327 327
FT CARBOHYD 351 351
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FT CARBOHYD 381 381
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FT CARBOHYD 400 400
FT CARBOHYD 435 435
FT CARBOHYD 450 450
FT CARBOHYD 458 458
FT CARBOHYD 598 598
FT CARBOHYD 603 603
FT CARBOHYD 612 612
FT CARBOHYD 624 624
FT CARBOHYD 803 803
FT SEQUENCE 843 AA; 95648 MW; C69D9D71C918B71 CRC64;
SQ
Query Match 65.1%; Score 82; DB 1; Length 843;
Best Local Similarity 54.5%; Pred. No. 5.9e-05;

Matches	12;	Conservative	5;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	1	LLSSWGCKGRIVCYTSVQMNST	22						
Db	579	LLGIWCGSGKILCTTTPMNTS	600						
RESULT 5									
ENV_HV11									
ID	ENV_HV11	STANDARD;	PRT;	847	AA.				
AC	ENV_HV11	STANDARD;	PRT;	847	AA.				
DT	01-FEB-1991	(Rel. 17, Created)							
DT	01-FEB-1991	(Rel. 17, Last sequence update)							
DT	15-JUL-1999	(Rel. 38, Last annotation update)							
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].								
DE	glycoprotein (GP120); Transmembrane glycoprotein (GP41)].								
GN	ENV.								
OS	Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).								
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.								
NCBI	TaxID=11691;								
[1]									
SEQUENCE FROM N.A.									
RX	MEDLINE=90347035; PubMed=2384920;								
RA	Cheng-Mayer C., Quiriga M., Tung J.W., Levy J.								
RT	"Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";								
RL	J. Virol. 64:4390-4398(1990).								
CC	-----								
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CC	-----								
DR	EMBL; M65024; AAA45072.1; -.								
DR	HIV; M38428; ENV5SF162.								
DR	InterPro; IPR000328; Env GP41.								
DR	InterPro; IPR000777; GP120.								
DR	Pfam; PF00516; GP120.1.								
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.								
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.								
FT	SIGNAL	1	29						
FT	CHAIN	30	502						
FT	CHAIN	503	847						
FT	DISULFID	53	73						
FT	DISULFID	118	203						
FT	DISULFID	125	194						
FT	DISULFID	130	155						
FT	DISULFID	216	245						
FT	DISULFID	226	237						
FT	DISULFID	294	328						
FT	DISULFID	374	435						
FT	DISULFID	381	408						
FT	CARBOHYD	87	87						
FT	CARBOHYD	135	135						
FT	CARBOHYD	154	154						
FT	CARBOHYD	186	186						
FT	CARBOHYD	195	195						
FT	CARBOHYD	222	232						
FT	CARBOHYD	239	239						
FT	CARBOHYD	260	260						
FT	CARBOHYD	274	274						
FT	CARBOHYD	293	293						
FT	CARBOHYD	299	299						
FT	CARBOHYD	329	329						
FT	CARBOHYD	336	336						
FT	CARBOHYD	352	352						
FT	CARBOHYD	382	382						
FT	CARBOHYD	388	388						
FT	CARBOHYD	392	392						
FT	CARBOHYD	392	392						
FT	CARBOHYD	392	392						

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FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96135 MW; 0A901317DF2AB CRC64;

Query Match 65.1%; Score 82; DB 1; Length 847;
Best Local Similarity 54.5%; Pred. No. 5,9e-05;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 583 LLSGCGSGKILCTTAVPMNAS 604
1 LLSGCGSGRLVCTSYQVNMNST 22
||| ||| ||| ||| |||
OY

RESULT 6
ENV_HV1W2 STANDARD; PRT; 847 AA.
ID ENV_HV1W2 STANDARD; PRT; 847 AA.
AC POS880:
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
CN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS.";
RL Sequence 232:1548-1553(1986).
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC
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CC -----
CC EMBL; M12507; AAB12990.1; -.
DR HIV; M12507; ENV5WMJ2.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KM signal.
KM signal.
FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 30 501 TRANSMEMBRANE GLYCOPROTEIN.
FT CHAIN 502 847
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 202 BY SIMILARITY.
FT DISULFID 125 193 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 225 326 BY SIMILARITY.
FT DISULFID 293 435 BY SIMILARITY.
FT DISULFID 372 435 BY SIMILARITY.
FT DISULFID 379 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 847 AA; 96466 MW; CDIE33D73AASBSCAE CRC64;

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Query Match 65.1%; Score 82; DB 1; Length 847;
Best Local Similarity 54.5%; Pred. No. 5.9e-05;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY 1 LLSWGCKGRLYCTYSVQNMST 22
583 LLSWGCKGRLYCTYSVQNMST 604

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RESULT 7
ENV_HV1B8 STANDARD; PRT; 851 AA.
ID ENV_HV1B8
AC P04582;
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Liyak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Ratajski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; K02011; AAA44661.1; -
CC
CC HVL; K02011; ENVSBB.
CC
CC GlycosubitedB; P04582; -

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DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 506
FT CHAIN 507 851
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 440
FT DISULFID 385 413
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
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FT CARBOHYD 443 443
FT CARBOHYD 458 458
FT CARBOHYD 606 606
FT CARBOHYD 611 611
FT CARBOHYD 620 620
FT CARBOHYD 632 632
FT CARBOHYD 669 669
FT CARBOHYD 745 745
FT CARBOHYD 811 811
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

```

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Query Match 65.1%; Score 82; DB 1; Length 851;
Best Local Similarity 54.5%; Pred. No. 5.9e-05;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY 1 LLSWGCKGRLYCTYSVQNMST 22
587 LLSWGCKGRLYCTYSVQNMST 608

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RESULT 8
ENV_HV1B8 STANDARD; PRT; 852 AA.
ID ENV_HV1B8
AC P12488;
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Liyak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Ratajski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).

```

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; K02011; AAA44661.1; -
CC
CC HVL; K02011; ENVSBB.
CC
CC GlycosubitedB; P04582; -

```

Accession	Protein	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score	DB 261	
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Cy		1	LLSSWGCKGRPLVCTSYQWVNST 22	
Dd		588	LLGIWGCGSKKICTTAVPMNNS 609	
 RESULT 9				
ID	_ENV_HV1S3	STANDARD;	PRT;	852 AA.
AC	PI9549;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [consists: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	Env.			
OS	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).			
OC	Vitruvius; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11690;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90317906; PubMed=2370688;			
RA	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;			
RT	"Human immunodeficiency virus type 1 cellular host range,			
RT	replication, and cytopathicity are linked to the envelope region of			
RL	the viral genome.";			
RL	J. Virol. 64:4016-4020(1990).			
CC	-----			
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CC	the European Bioinformatics institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.ebi.ac.uk/announcements/			
CC	or send an email to license@ebi-sib.ch).			
CC	-----			
DR	EMBL; M38427; AAA45067.1; .			
DR	HIV; M38427; ENVSEF33.			
DR	InterPro: IPR000328; Env GP41.			
DR	InterPro: IPR000772; GP120.			
DR	Pfam; PF00515; GP41_1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	SIGNAL	1	31	BY SIMILARITY.
FT	CHAIN	32	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	852	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	156	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	331	BY SIMILARITY.
FT	DISULFID	377	439	BY SIMILARITY.
FT	DISULFID	384	412	BY SIMILARITY.
FT	CARBOHYD	87		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	159	159	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	189	189	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	277	277	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	339	339	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 9663 MW; E87BF8D23C9910D CRC64;

Query Match 65.1%; Score 82; DB 1; Length 852;
Best Local Similarity 54.5%; Pred. No. 5.9e-05;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTSVQMNST 22
588 LLGIWGCGRKLCITTVPMNNTS 609

RESULT 10
ENV_HV1MF STANDARD; PRT; 853 AA.
AC P19551;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C.,
RA Maclak A.;
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis."
RL J. Virol. 64:3792-3803(1990).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL; M33943; AAA44850.1; -.
DR HIV; M33943; ENVSMFA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00515; GP120.1.
DR Pfam; PF00517; GP41.1.
DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
RW signal.
FT SIGNAL 1 30
FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 54 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 203 BY SIMILARITY.
FT DISULFID 126 194 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 329 BY SIMILARITY.
FT DISULFID 376 443 BY SIMILARITY.

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FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 65.1%; Score 82; DB 1; Length 853;
Best Local Similarity 54.5%; Pred. No. 5.9e-05;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTSVQMNST 22
590 LLGIWGCGRKLCITTVPMNNTS 611

RESULT 11
ENV_HV1A2 STANDARD; PRT; 855 AA.
AC P03378;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2)."
RL Science 227:484-492(1985).
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CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL; K02007; AAB59882.1; -.

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DR PIR: A03976; VCLJN2.
 DR HIV: K02007; ENV58F2.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120, 1.
 DR Pfam: PF00517; GP41, 1.
 DR Aids: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 signal.
 FT SIGNAL 1 29
 FT CHAIN 30 509
 FT CHAIN 510 855
 FT DISULFID 53 73
 FT DISULFID 118 208
 FT DISULFID 125 199
 FT DISULFID 130 155
 FT DISULFID 221 250
 FT DISULFID 231 242
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 FT SEQUENCE 855 AA; 97438 MW; A3BC20573AAC1A2 CRC64;
 SQ

Query Match 65.1%; Score 82; DB 1; Length 855;
 Best Local Similarity 54.5%; Pred. No. 5.9e-05;
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCGRLVCTYSVQNST 22
 Db 591 LIGWGCGKLCITTAVPNMS 612

RESULT 12
 ENV_HV10Y STANDARD; PRT; 855 AA.
 AC P20888;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).

CC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90146544; PubMed=2559749;
 RA Huot T, Daza M.C., Brun-Vezinet F., Roelants G.B., Wain-Hobson S.;
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
 individual presenting an atypical western blot.";
 RL Aids 3:707-715(1989).
 CC -1- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A
 HEALTHY GABONESE INDIVIDUAL.
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 or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: M26727; AAA83397.1; -.
 DR HIV: M26727; ENV50YI.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120, 1.
 DR Pfam: PF00517; GP41, 1.
 DR Aids: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 signal.
 FT SIGNAL 1 29
 FT CHAIN 30 509
 FT CHAIN 510 855
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
 FT DISULFID 381 442
 FT DISULFID 388 415
 FT CARBOHYD 87 87
 FT CARBOHYD 134 134
 FT CARBOHYD 142 142
 FT CARBOHYD 145 145
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
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 FT CARBOHYD 202 202
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 FT CARBOHYD 267 267
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 FT CARBOHYD 636 636
 FT CARBOHYD 815 815
 FT SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CRC64;
 SQ

Query Match 65.1%; Score 82; DB 1; Length 855;
 Best Local Similarity 54.5%; Pred. No. 5.9e-05;
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy		1	L1SSMGCKRGLVCTYSVOAMN 22	
Dd		591	L1GIWGGSGKLICTTIVPMNAS 612	
RESULT 13				
ENV_HVIB1				
ID	ENV_HVIB1	STANDARD;	PRT,	856 AA.
AC	P03375;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	Envelope polypeptide Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11678;			
RN	[1]			
	SEQUENCE FROM N.A.			
	MEDLINE=8511123; PubMed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petesky S.R. Jr., Pearson M.L., Laurenceberg J.A., Papas T.S., Chetty J., Chang N.T., Gallo R.C., Wong-Staal F.;			
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RL	Nature 313:277-284(1985).			
RN	[2]			
RP	DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.			
RX	MEDLINE=90285159; PubMed=2355006;			
SA	Leonard C.K., Spellman M.W., Riddle L., Harris R.U., Thomas J.N., Gregory T.J.;			
RT	"Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in Chinese hamster ovary cells";			
RT	J. Biol. Chem. 265:10373-10382(1990).			
CC	-----			
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CC	-----			
EMBL:	M15654; AAA44205.1; -			
PIR:	A03973; VCLJH3.			
HIV:	M15654; ENVSHB102.			
DR	InterPro: IPR000328; Env GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00517; GP41; 1.			
DR	Pfam: PF00517; GP41; 1.			
Kw	Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL.	1	30	
FT	CHAIN	1	511	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	512	856	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	
FT	DISULFID	119	205	
FT	DISULFID	126	196	
FT	DISULFID	131	157	
FT	DISULFID	218	247	
FT	DISULFID	228	239	
FT	DISULFID	296	331	
FT	DISULFID	378	445	
FT	CARBOHYD	385	418	
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. . .)

[illegible]

Query Match 65.1%; Score 82; DB 1; Length 856;
 Best Local Similarity 54.5%; Pred. No. 6e-05;
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 LLSWGCKGRLVCYTSVQMNST 22
 |||||:|:|:|:|:
 Db 592 LIGIWGCSGKLICTTAVPWNAS 613

Search completed: May 29, 2003, 10:36:58
 Job time : 5.4127 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:32:35 ; Search time 22.6984 Seconds
(without alignments)
199.707 Million cell updates/sec

Title: US-09-147-362A-4

Perfect score: 126
Sequence: 1 LLSWGCKGRLVCTSVQWNST 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	92.1	219	15 Q91EB6	Q91EB6 human immun
2	115	91.3	135	15 Q9DQL9	Q9DQL9 human immun
3	115	91.3	216	15 Q91EC5	Q91EC5 human immun
4	115	91.3	218	15 Q91E95	Q91E95 human immun
5	115	91.3	242	15 Q91E31	Q91E31 human immun
6	115	91.3	538	15 Q91ED5	Q91ED5 human immun
7	113	89.7	214	15 Q91DK3	Q91DK3 human immun
8	113	89.7	214	15 Q91EC7	Q91EC7 human immun
9	113	89.7	234	15 Q91E26	Q91E26 human immun
10	113	89.7	535	15 Q91EF2	Q91EF2 human immun
11	113	89.7	551	15 Q91EB1	Q91EB1 human immun
12	112	88.9	116	15 O11941	O11941 human immun
13	112	88.9	116	15 O40458	O40458 human immun
14	112	88.9	130	15 Q91HU9	Q91HU9 human immun
15	112	88.9	183	15 Q91EC1	Q91EC1 human immun
16	112	88.9	220	15 Q91EC9	Q91EC9 human immun

17	112	88.9	235	15 Q91E54	Q91E54 human immun
18	112	88.9	512	15 Q91ED2	Q91ED2 human immun
19	112	88.9	872	15 Q8Q7H0	Q8Q7H0 human immun
20	112	88.9	879	15 Q9W1U9	Q9W1U9 human immun
21	112	88.9	880	15 Q8Q7I9	Q8Q7I9 human immun
22	112	88.9	882	15 Q8Q7F9	Q8Q7F9 human immun
23	112	88.9	887	15 Q8Q7H6	Q8Q7H6 human immun
24	112	88.9	887	15 Q8Q7G9	Q8Q7G9 human immun
25	112	88.9	900	15 Q9QNZ8	Q9QNZ8 human immun
26	111	88.1	114	15 O40448	O40448 human immun
27	111	88.1	209	15 Q91E66	Q91E66 human immun
28	110	87.3	218	15 O40451	O40451 human immun
29	110	87.3	214	15 Q91E96	Q91E96 human immun
30	110	87.3	216	15 Q91E45	Q91E45 human immun
31	110	87.3	219	15 Q91EC8	Q91EC8 human immun
32	110	87.3	242	15 Q91E30	Q91E30 human immun
33	110	87.3	544	15 Q91ED9	Q91ED9 human immun
34	110	87.3	548	15 Q91ED6	Q91ED6 human immun
35	110	87.3	865	15 Q8Q7H7	Q8Q7H7 human immun
36	110	87.3	867	15 Q8Q7G8	Q8Q7G8 human immun
37	109	86.5	116	15 O40459	O40459 human immun
38	109	86.5	118	15 Q9E5S0	Q9E5S0 human immun
39	109	86.5	119	15 Q91HU5	Q91HU5 human immun
40	109	86.5	121	15 Q91HV7	Q91HV7 human immun
41	109	86.5	134	15 Q91HV4	Q91HV4 human immun
42	109	86.5	137	15 Q91HV5	Q91HV5 human immun
43	109	86.5	146	15 Q9WRV2	Q9WRV2 human immun
44	109	86.5	200	15 Q91EB8	Q91EB8 human immun
45	109	86.5	227	15 Q91E99	Q91E99 human immun

ALIGNMENTS

RESULT 1

Q91EB6 PRELIMINARY; PRT; 219 AA.

AC Q91EB6; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp41 (Fragment) %
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.:
RC STRAIN=BCR14;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ236404; CAB96252.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

Query Match 92.1%; Score 116; DB 15; Length 219;
Best Local Similarity 86.4%; Pred. No. 2.4e-10;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCTSVQWNST 22
||:|||||:|||||:|||||:
Db 57 LLSWGCKGRLVCTSVQWNST 78

RESULT 2
Q9DQL9 PRELIMINARY; PRT; 135 AA.

AC Q9DOL9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP-M1321;
RA MEDLINE=20584646; PubMed=1153079;
RA Ortiz M., Munoz L., Bernal A., Rodriguez A.,
RA Vellido J., Salas A., Moreno A., Garcia-Saiz A.,
RT "Molecular Characterization of Non-B HIV Type 1 Subtypes from Africa
RT in Spain".
RL AIDS Res. Hum. Retroviruses 16:1967-1971(2000).
DR EMBL; AF255939; AG36894.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 16285 MW; D34B9EF77318B36 CRC64;

Query Match 91.3%; Score 115; DB 15; Length 135;
Best Local Similarity 81.8%; Pred. No. 2.4e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLSWGCKGRIVCYTSVKNST 22
DB 48 LLSWGCKGRIVCYTSVKNST 69

RESULT 3
Q9IEC3
ID Q9IEC3 PRELIMINARY; PRT; 216 AA.
AC Q9IEC3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF07;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AJ236394; CAB96243.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 216 216
SQ SEQUENCE 216 AA; 25027 MW; 413AB9BBF1B4FC9A CRC64;

Query Match 91.3%; Score 115; DB 15; Length 216;
Best Local Similarity 86.4%; Pred. No. 3.4e-10;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 LLSWGCKGRIVCYTSVKNST 22
DB 47 LLSWGCKGRIVCYTSVKNST 68

RESULT 4
Q9IEB5

ID Q9IEB5 PRELIMINARY; PRT; 218 AA.
AC Q9IEB5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7BF51;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AJ236425; CAB96273.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 25243 MW; E7F0B1E20EF79FA8 CRC64;

Query Match 91.3%; Score 115; DB 15; Length 218;
Best Local Similarity 81.8%; Pred. No. 3.4e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLSWGCKGRIVCYTSVKNST 22
DB 54 LLSWGCKGRIVCYTSVKNST 75

RESULT 5
Q9IEB1
ID Q9IEB1 PRELIMINARY; PRT; 242 AA.
AC Q9IEB1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TM, GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF112;
RA Roques P., Robertson D., Souquiere S., Diamond F., Mauchere P.,
RA Depienne C., Brun-Vezinet F., Dormont D., Simon F.O.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AJ243366; CAB96336.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 242 242
SQ SEQUENCE 242 AA; 27539 MW; DE8A73DF0E8A6FD7 CRC64;

Query Match 91.3%; Score 115; DB 15; Length 242;
Best Local Similarity 81.8%; Pred. No. 3.8e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLSWGCKGRIVCYTSVKNST 22
DB 64 LLSWGCKGRIVCYTSVKNST 85

RESULT 6
Q9IEB5 PRELIMINARY; PRT; 538 AA.

AC Q91ED5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 19, Last annotation update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP STRAIN=YBP51;
RC STRAIN=YBP51;
RA Roques P., Robertson D., Darnold F., Souquiere S., Mauclele P.,
RA Deleigne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-GP41 region."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133072; CAB96233.1; -
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 538
SQ SEQUENCE 538 AA; 60777 MW; B3C9E66A23FEFID CRC64;

Query Match 91.3%; Score 115; DB 15; Length 538;
Best Local Similarity 81.8%; Pred. No. 8.5e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRVCTSVQNMST 22
DB 374 LLSWGCKGRVCTSVQNMST 395

RESULT 7
Q9DIK3 PRELIMINARY; PRT; 214 AA.
AC Q9DIK3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GP41 protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP STRAIN=BCE120;
RC STRAIN=BCE120;
RA Roques P., Robertson D., Darnold F., Souquiere S., Mauclele P.,
RA Deleigne C., Brun-Vezinet F., Dormont D., Simon P.;
RT "Phylogenetic analysis of 49 newly derived HIV-1 group O strains: High
RT viral diversity but no group M-like subtypes."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ298125; CAB18806.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 24436 MW; FFA990D08F81AB CRC64;

Query Match 89.7%; Score 113; DB 15; Length 214;
Best Local Similarity 81.8%; Pred. No. 6.9e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRVCTSVQNMST 22
DB 45 LLSWGCKGRVCTSVQNMST 66

ID Q91EC7 PRELIMINARY; PRT; 216 AA.
AC Q91EC7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP STRAIN=BCEP03;
RC STRAIN=BCEP03;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ236392; CAB96241.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 25015 MW; 780C5F39CA697C2 CRC64;

Query Match 89.7%; Score 113; DB 15; Length 216;
Best Local Similarity 86.4%; Pred. No. 7e-10;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRVCTSVQNMST 22
DB 55 LLSWGCKGRVCTSVQNMST 76

RESULT 9
Q91EAG PRELIMINARY; PRT; 234 AA.
AC Q91EAG;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP STRAIN=YBP22;
RC STRAIN=YBP22;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ236414; CAB96262.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 234
SQ SEQUENCE 234 AA; 26737 MW; 34CFDBE999DEFB82 CRC64;

Query Match 89.7%; Score 113; DB 15; Length 234;
Best Local Similarity 86.4%; Pred. No. 7.5e-10;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRVCTSVQNMST 22
DB 62 LLSWGCKGRVCTSVQNMST 83

RESULT 8

RESULT 10

ID Q9IEF2 PRELIMINARY; PRT; 535 AA.
AC Q9IEF2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
NM [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BCF03;
RA Rognes P., Robergson D., Diamond F., Souquiere S., Mauciere P.,
Deleigne C., Brun-Vezinet F., Dormont D.,
"HIV-1 group O phylogenetic analysis of C2-gp41 region."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133055; CAB96216.1; -
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
PFam; PF00517; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT SEQUENCE 535 AA; 59682 MW; 7234BB8378DD12C5 CRC64;
SQ

Query Match 89.7%; Score 113; DB 15; Length 535;
Best Local Similarity 86.4%; Pred. No. 1.7e-09;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRILVCTSVQNMST 22
Db 374 LLSWGCKGRILVCTSVQNMST 395

RESULT 11
Q9IEE1 PRELIMINARY; PRT; 551 AA.
ID Q9IEE1;
AC Q9IEE1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
NM [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=YBF2;
RA Rognes P., Robergson D., Diamond F., Souquiere S., Mauciere P.,
Deleigne C., Brun-Vezinet F., Dormont D.,
"HIV-1 group O phylogenetic analysis of C2-gp41 region."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133056; CAB96227.1; -
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
PFam; PF00517; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT SEQUENCE 551 AA; 61704 MW; 1CF824CAD5A89ECF CRC64;
SQ

Query Match 89.7%; Score 113; DB 15; Length 551;
Best Local Similarity 86.4%; Pred. No. 1.8e-09;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRILVCTSVQNMST 22
Db 379 LLSWGCKGRILVCTSVQNMST 400

RESULT 12
ID O11941 PRELIMINARY; PRT; 116 AA.
AC O11941;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
NM [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ABR124;
RX MEDLINE=97340911; PubMed=9197385;
RA Brennan C.A., Hackett J. Jr., Zekeng L., Lund J.K., Vallari A.S.,
Hickman R.K., Gurtler L., Kapue L., von Overbeck J., Hampf H.,
Devere S.G.,
"Sequence of gp41env immunodominant region of HIV type 1 group O from
west Central Africa."
RL AIDS Res. Hum. Retroviruses 13:901-904(1997).
DR EMBL; U90134; AAB62817.1; -
DR InterPro; IPR000328; Env GP41.
PFam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT SEQUENCE 116 AA; 13789 MW; 488A9A40F4255E3E CRC64;
SQ

Query Match 88.9%; Score 112; DB 15; Length 116;
Best Local Similarity 81.8%; Pred. No. 5.3e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRILVCTSVQNMST 22
Db 39 LLSWGCKGRILVCTSVQNMST 60

RESULT 13
ID O40458 PRELIMINARY; PRT; 116 AA.
AC O40458;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE Envelope transmembrane glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
NM [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=GROUP O;
RA Biolley-Ruche F., Ekasa E., Peeters M., Delaporte E.,
"Molecular characterization of envelope transmembrane glycoprotein of
RT 14 new human immunodeficiency virus type 1 group O strains from
different African countries."
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y09774; CAA70913.1; -
DR InterPro; IPR000328; Env GP41.
PFam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT SEQUENCE 116 AA; 13865 MW; 540F5B3B7AD849D8 CRC64;
SQ

Query Match 88.9%; Score 112; DB 15; Length 116;
Best Local Similarity 81.8%; Pred. No. 5.3e-10;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLSWGCKGRILVCTSVQNMST 22
Db 39 LLSWGCKGRILVCTSVQNMST 60

DB 39 LNLWGCCKRLCYTSVQMNKT 60

RESULT 14

Q9IHU9 PRELIMINARY; PRT; 130 AA.
 AC Q9IHU9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN GP41.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97CW798;
 RX MEDLINE=20386754; PubMed=10933623;
 P Yang C., Gao F., Fontjuno P.N., Zekeng L., van der Groen G.,
 Pleniakzek D., Schable C., Lal R.B.;
 "Phylogenetic analysis of protease and transmembrane regions of HIV
 type 1 group O."
 RT AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
 DR EMBL: AF229235; AAF71912.1;
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 130 AA; 15593 MW; 5385789A336344EA CRC64;

Query Match 88.9%; Score 112; DB 15; Length 130;
 Best Local Similarity 81.8%; Pred. No. 6e-10;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSWGCKRLCYTSVQMNST 22
 Db 40 LLSWGCKRLCYTSVQMNKT 61

RESULT 15

Q9IECI PRELIMINARY; PRT; 183 AA.
 AC Q9IECI;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 GN GP41 (Fragment).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCF101;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ236398; CAB96247.1;
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 183 AA; 21722 MW; C22A28A73540C8AA CRC64;

Query Match 88.9%; Score 112; DB 15; Length 183;
 Best Local Similarity 81.8%; Pred. No. 8.4e-10;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSWGCKRLCYTSVQMNST 22

DB 42 LNLWGCCKRLCYTSVQMNST 63

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 Job time : 23.6984 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20 ; Search time 29.3333 Seconds
(without alignments)
99.938 Million cell updates/sec

Title: US-09-147-362A-5

Perfect score: 127
Sequence: 1 LLOGMCKGRIVCTYSVQMNST 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	100.0	22	19	AAW80463
2	122	96.1	22	19	AAW80462
3	118	97.9	22	19	AAW80461
4	115	90.6	22	19	AAW80466
5	114	88.8	40	17	AAW07346
6	112	88.2	40	17	AAW07352
7	111	87.4	32	19	AAW80469
8	111	87.4	41	17	AAW07351
9	111	87.4	113	20	AAV05565
10	111	87.4	715	20	AAV05625

11	110	86.6	33	21	AAW12212	Partial sequence o
12	109	86.6	113	20	AAV05559	HIV-1 group O isol
13	109	85.8	22	19	AAW80460	Peptide derived fr
14	109	85.8	33	21	AAW12231	Partial sequence o
15	109	85.8	40	17	AAW07343	Partial sequence o
16	109	85.8	40	17	AAW07344	Partial sequence o
17	109	85.8	41	17	AAW07353	Partial sequence o
18	109	85.8	117	20	AAV05548	HIV-1 group O isol
19	108	85.0	116	20	AAV05555	HIV-1 group O isol
20	107	84.3	22	19	AAW80464	Peptide derived fr
21	107	84.3	23	20	AAV05623	HIV-1 group O extra
22	107	84.3	33	21	AAW12236	Partial sequence o
23	107	84.3	113	20	AAV05551	HIV-1 group O isol
24	107	84.3	113	20	AAV05550	HIV-1 group O isol
25	107	84.3	200	21	AAV77373	HIV-1 group O env
26	107	84.3	215	20	AAV09499	HIV-1 group O env
27	107	84.3	215	20	AAV06983	Recombinant pGO-8P
28	107	84.3	215	21	AAV77374	HIV-1 group O env
29	107	84.3	245	20	AAV09493	HIV-1 group O env
30	107	84.3	245	20	AAV06977	Recombinant pGO-9P
31	107	84.3	245	21	AAV77369	HIV-1 group O pGO-
32	107	84.3	281	20	AAV09507	HIV-1 group O env
33	107	84.3	373	20	AAV09495	HIV-1 group O env
34	107	84.3	373	20	AAV06979	Recombinant pGO-11
35	107	84.3	460	20	AAV09500	Recombinant pGO-8C
36	107	84.3	460	20	AAV06984	HIV-1 group O env
37	107	84.3	460	21	AAV77375	HIV-1 group O env
38	107	84.3	474	21	AAV77371	HIV-1 group O env
39	107	84.3	488	20	AAV09504	HIV-1 group M and
40	107	84.3	490	20	AAV09494	HIV-1 group O env
41	107	84.3	490	20	AAV06978	Recombinant pGO-9C
42	107	84.3	490	21	AAV77370	HIV-1 group O env
43	107	84.3	526	20	AAV09505	HIV-1 group O poly
44	107	84.3	618	20	AAV09496	HIV-1 group O env
45	107	84.3	618	20	AAV06980	Recombinant pGO-11

ALIGNMENTS

RESULT 1

AAW80463

ID AAW80463 standard; peptide; 22'AA.

XX AAW80463;

AC AAW80463;

XX 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

KW

XX Synthetic

OS Immune deficiency virus.

OS

XX W09845323-A1.

PN 15-OCT-1998.

XX

PD 06-APR-1998; 98WO-FR00691.

XX

PF 24-FEB-1998; 98FR-0002212.

XX

PR 09-APR-1997; 97FR-0004356.

XX

XX (SNP) PASTEUR SANOFI DIAGNOSTICS SA.

PA

XX Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

PI WPI; 1998-583190/49.

XX

DR

XX New synthetic peptide(s) - useful for, e.g. detecting infection by

PT human immune deficiency virus of group O

XX

PS Claim 6; Page 42; 55pp; French.
 CC AAM80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 127; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5e-10; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

QY 1 LLOSNGCKGRLVCTSVQMNST 22
 DB 1 LLOSNGCKGRLVCTSVQMNST 22

ULT 2

AAW80462
 ID AAW80462 standard; peptide; 22 AA.

XX AAW80462;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.

OS Immune deficiency virus.

XX WO9845323-A1.

XX 15-OCT-1998.

PD 06-APR-1998; 98WO-FR00691.

XX 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PA Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

XX WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX

SQ Sequence 22 AA;

Query Match 96.1%; Score 122; DB 19; Length 22;
 Best Local Similarity 95.5%; Pred. No. 2.2e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRLVCTSVQMNST 22
 DB 1 LLOSNGCKGRLVCTSVQMNST 22

RESULT 3
 AAW80461
 ID AAW80461 standard; peptide; 22 AA.

XX AAW80461;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.

OS Immune deficiency virus.

XX WO9845323-A1.

XX 15-OCT-1998.

PD 06-APR-1998; 98WO-FR00691.

XX 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PA Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

XX WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O

XX Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX

SQ Sequence 22 AA;

Query Match 92.9%; Score 118; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 7.5e-09;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRLVCTSVQMNST 22
 DB 1 LLOSNGCKGRLVCTSVQMNST 22

RESULT 4
 AAW80466
 ID AAW80466 standard; peptide; 22 AA.

XX AAW80466;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.

OS Immune deficiency virus.

XX WO9845323-A1.

XX 15-OCT-1998.

PD 06-APR-1998; 98WO-FR00691.

```

XX 24-FEB-1998; 98FR-0002212.
PR 09-APR-1997; 97FR-0004356.
XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.
XX
XX Cheneboux DMB, Delagneau JFH, Gabelle SJX, Riennier FY,
XX WPI; 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 43; 55pp; French.
XX
XX AAM80459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O
XX human immune deficiency virus (HIV).
XX
SQ Sequence 22 AA;
Query Match 90.6%; Score 115; DB 19; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.9e-08;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 LLSWGCKGRIVCYTSVQNMST 22
Db 1 LLSWGCKGRIVCYTSVQNMST 22
RESULT 5
AAM07346
ID AAM07346 standard; peptide; 40 AA.
XX
XX AAM07346;
XX
XX 03-JUN-1997 (first entry)
XX
XX Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).
XX
XX Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;
XX C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
XX primer; hybridisation; amplification; PCR; polymerase chain reaction;
XX immunogen; antibody.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO9627013-A1.
XX
XX 06-SEP-1996.
XX
XX 26-FEB-1996; 96WO-FR00294.
XX
XX 27-FEB-1995; 95FR-0002236.
XX
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Chaix-Baudier ML, Lousseret-Ajaka I, Ly T, Saragosti S, Simon F;
XX WPI; 1996-412779/41.
XX
XX N-PSDB; AA144922.
XX
XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
XX antibodies - useful for diagnosis, screening and typing, or as
XX immunogens
XX
XX Claim 12; Page 34; 71pp; French.
XX
XX Human immunodeficiency virus type 1 (HIV-1) strains are currently

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CC divided into 2 major groups based on the nucleotide sequences of the
CC envelop gene (env): group M containing sub-groups A-G, and group O
CC containing the strains ANR70 and MWP5180. The invention relates to the
CC discovery of several new strains of HIV-1 which can be placed in group O,
CC based on the partial sequences of the C2V3-env, gp41 and gag genes (see
CC AAT44907-39 and AAM07329-64). The novel strains have been deposited as
CC retroviruses CNCM 1-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07
CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
CC presented here is from the strain BCF07 (MAN) and corresponds to a
CC fragment of the gp41 protein encoded by the env gene. The nucleic acids
CC can be used to detect gp. O HIV-1 strains by hybridisation or (as
CC primers) by gene amplification, also for screening and typing of such
CC strains. Peptides encoded by the nucleic acids can be used as immunogens
CC to raise Ab for detecting gp. O HIV-1.
XX
SQ Sequence 40 AA;
Query Match 89.8%; Score 114; DB 17; Length 40;
Best Local Similarity 86.4%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 LLSWGCKGRIVCYTSVQNMST 22
Db 19 LLSWGCKGRIVCYTSVQNMST 40
RESULT 6
AAM07352
ID AAM07352 standard; peptide; 40 AA.
XX
XX AAM07352;
XX
XX 03-JUN-1997 (first entry)
XX
XX Partial sequence of gp41 from HIV-1 gp. O strain BCF13.
XX
XX Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;
XX C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
XX primer; hybridisation; amplification; PCR; polymerase chain reaction;
XX immunogen; antibody.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO9627013-A1.
XX
XX 06-SEP-1996.
XX
XX 26-FEB-1996; 96WO-FR00294.
XX
XX 27-FEB-1995; 95FR-0002236.
XX
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Chaix-Baudier ML, Lousseret-Ajaka I, Ly T, Saragosti S, Simon F;
XX WPI; 1996-412779/41.
XX
XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
XX antibodies - useful for diagnosis, screening and typing, or as
XX immunogens
XX
XX Claim 12; Page 46; 71pp; French.
XX
XX Human immunodeficiency virus type 1 (HIV-1) strains are currently
XX divided into 2 major groups based on the nucleotide sequences of the
XX envelop gene (env): group M containing sub-groups A-G, and group O
XX containing the strains ANR70 and MWP5180. The invention relates to the
XX discovery of several new strains of HIV-1 which can be placed in group O,
XX based on the partial sequences of the C2V3-env, gp41 and gag genes (see
XX AAT44907-39 and AAM07329-64). The novel strains have been deposited as
XX retroviruses CNCM 1-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07
XX (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence

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CC presented here is from the strain BCF13 and corresponds to a fragment of
 CC the gp41 protein encoded by the env gene. The nucleic acids can be used
 CC to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene
 CC amplification, also for screening and typing of such strains. Peptides
 CC encoded by the nucleic acids can be used as immunogens to raise Ab for
 CC detecting gp. O HIV-1.

XX Sequence 40 AA;

Query Match 88.2%; Score 112; DB 17; Length 40;

Best Local Similarity 86.4%; Pred. No. 8e-08; Mismatches 2; Indels 0; Gaps 0;

DB 1 LLSWGCKGRLVCTYSVMNST 22
 19 LLSWGCKGRLVCTYSVMNST 40

RESULT 7

AAW0469 standard; peptide; 32 AA.

AC AAW0469;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

XX WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagrange JFH, Gadelie SJX, Rieunier FY;

DR WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by
 human immune deficiency virus of group O

PS Claim 6; Page 44; 55pp; French.

XX AAW0459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).

XX Sequence 32 AA;

Query Match 87.4%; Score 111; DB 19; Length 32;

Best Local Similarity 81.8%; Pred. No. 8.8e-08; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCTYSVMNST 22
 11 LLSWGCKGRLVCTYSVMNST 32

RESULT 8

AAW07351

ID AAW07351 standard; peptide; 41 AA.

AC AAW07351;

DT 03-JUN-1997 (first entry)

DE Partial sequence of gp41 from HIV-1 gp. O strain BCF12.

XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
 XX C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
 XX primer; hybridisation; amplification; PCR; polymerase chain reaction;
 XX immunogen; antibody.

OS Human immunodeficiency virus type 1.

XX WO9627013-A1.

PD 06-SEP-1996.

PF 26-FEB-1996; 96WO-FR00294.

PR 27-FEB-1995; 95FR-0002236.

PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

PI (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Chailx-Baudier ML, Lousset-Ayaka I, Ly T, Saragosti S, Simon F;

DR WPI; 1996-412779/41.

PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 PT immunogens

PS Claim 12; Page 46; 71pp; French.

XX Human immunodeficiency virus type 1 (HIV-1) strains are currently
 CC divided into 2 major groups based on the nucleotide sequences of the
 CC envelope gene (env): group M containing sub-groups A-G, and group O
 CC containing the strains ANR70 and MWP5180. The invention relates to the
 CC discovery of several new strains of HIV-1 which can be placed in group O,
 CC based on the partial sequences of the C2V3-env, gp41 and gag genes (see
 CC AAT44907-39 and AAW07328-64). The novel strains have been deposited as
 CC retroviruses CMCN T-1544 (BCF02 (BSS)), 1543 (BCF01 (FAN)), 1546 (BCF07
 CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
 CC presented here is from the strain BCF12 and corresponds to a fragment of
 CC the gp41 protein encoded by the env gene. The nucleic acids can be used
 CC to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene
 CC amplification, also for screening and typing of such strains. Peptides
 CC encoded by the nucleic acids can be used as immunogens to raise Ab for
 CC detecting gp. O HIV-1.

XX Sequence 41 AA;

Query Match 87.4%; Score 111; DB 17; Length 41;

Best Local Similarity 81.8%; Pred. No. 1.1e-07; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCTYSVMNST 22
 19 LLSWGCKGRLVCTYSVMNST 40

RESULT 9

AAV05565

ID AAV05565 standard; Protein; 113 AA.

AC AAV05565;

DT 19-JUL-1999 (first entry)

DE HIV-1 group O isolate MP539-PBWC gp41 antigen.

KM HIV-1 group O: Outlier strain; gp41; envelope protein; antigen;
 KM vaccine; diagnosis; AIDS.
 XX
 XX
 OS Human immunodeficiency virus type 1.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 65 /note= "encoded by AMK"
 FT Misc-difference 74 /note= "encoded by ATR"
 FT Misc-difference 84 /note= "encoded by GAK"
 FT Misc-difference 86 /note= "encoded by AGY"
 FT
 PN WO9904011-A2.
 XX
 PD 28-JAN-1999.
 XX
 XX 20-JUL-1998; 98WO-EP04522.
 XX
 XX 18-JUL-1997; 97EP-0870110.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
 XX
 DR WPI, 1999-132255/11.
 DR N-PSDB; AAY05565.
 XX
 PT New isolated HIV-1 group O strains - used to produce
 PT polynucleotides, antigens and antibodies for use in diagnosis and in
 PT vaccines for prevention of HIV-1 infection
 XX
 XX Claim 3; Fig 6; 162pp; English.
 XX
 CC The present sequence is an antigen of the gp41 protein of HIV-1
 CC group O (Outlier) strain MP539-FBMC, a Cameroon isolate. The
 CC invention relates to new HIV-1 group O antigens (see AAY05546-625),
 CC and the use of these antigens, or nucleic acids encoding them (see
 CC AAX25154-80), in the diagnosis and prophylaxis of AIDS. They can be
 CC used as reagents for detecting HIV-1 group O infection and for
 CC differentiating different types of HIV-1 group O infection.
 CC Vaccines that provide protective immunity against HIV-1 infection, in
 CC particular against HIV-1 group O infection, comprise at least one
 CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a
 CC virus-like particle comprising such an antigen, or an attenuated
 CC form of an HIV-1 type O strain. The invention also relates to new
 CC HIV-1 group O strains, mostly from patients from Cameroon and its
 CC neighbouring countries.
 XX
 SQ Sequence 113 AA;
 XX
 Query Match 87.4%; Score 111; DB 20; Length 113;
 Best Local Similarity 81.8%; Pred. No. 2.8e-07;
 Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 LLSQWCKGKRLVCTYSVQMNST 22
 DB 39 LLNLWGCKGRLLCTYSVQMNKT 60
 XX
 RESULT 10
 ID AAY05625 standard; Protein; 715 AA.
 XX
 AC AAY05625;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE HIV-1 group O isolate MP645 envelope protein (Env).
 XX
 KW HIV-1 group O; Outlier strain; envelope protein; Env; antigen;

KM vaccine; diagnosis; AIDS.
 XX
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9904011-A2.
 XX
 PD 28-JAN-1999.
 XX
 XX 20-JUL-1998; 98WO-EP04522.
 XX
 XX 18-JUL-1997; 97EP-0870110.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
 XX
 DR WPI, 1999-132255/11.
 DR N-PSDB; AAX25180.
 XX
 PT New isolated HIV-1 group O strains - used to produce
 PT polynucleotides, antigens and antibodies for use in diagnosis and in
 PT vaccines for prevention of HIV-1 infection.
 XX
 XX Claim 3; Fig 8A; 162pp; English.
 XX
 CC The present sequence is a partial Env polypeptide of HIV-1 group O
 CC (Outlier) virus isolate MP645, as deduced from part of the genome
 CC of MP645 (see AAX25180). The invention relates to new HIV-1 group O
 CC antigens, especially envelope protein antigens (see AAY05546-625),
 CC and the use of these antigens, or nucleic acids encoding them (see
 CC AAX25154-80), in the diagnosis and prophylaxis of AIDS. They can be
 CC used as reagents for detecting HIV-1 group O infection and for
 CC differentiating different types of HIV-1 group O infection.
 CC Vaccines that provide protective immunity against HIV-1 infection,
 CC in particular against HIV-1 group O infection, comprise at least
 CC one HIV-1 type O antigen, a nucleic acid encoding such an antigen,
 CC a virus-like particle comprising such an antigen, or an attenuated
 CC form of an HIV-1 type O strain. The invention also relates to new
 CC HIV-1 group O strains, obtained from patients from Cameroon, Gabon,
 CC Tchad, Nigeria, Senegal and Niger.
 XX
 SQ Sequence 715 AA;
 XX
 Query Match 87.4%; Score 111; DB 20; Length 715;
 Best Local Similarity 86.4%; Pred. No. 1.6e-06;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 LLSQWCKGKRLVCTYSVQMNST 22
 DB 628 LLNLWGCKGRLLCTYSVQMNRT 649
 XX
 RESULT 11
 ID AAB12212 standard; peptide; 33 AA.
 XX
 AC AAB12212;
 XX
 DT 10-NOV-2000 (first entry)
 XX
 DE Partial sequence of HIV-1 strain BCF13 gp41 immunodominant region.
 XX
 DE HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
 KW acquired immunodeficiency syndrome; group O HIV; gp41; BCF13.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN EP1013766-A2.
 XX
 PD 28-JUN-2000.
 XX
 PF 29-NOV-1999; 99EP-0309491.
 XX

PR 30-NOV-1998; 98US-0110292.
 PR 08-FEB-1999; 99US-0119138.
 PR 04-NOV-1999; 99US-0433428.
 XX
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 PI De Leye R, Zheng J;
 DR WPI; 2000-402205/35.
 XX
 PT New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PT virus group O antibodies -
 XX
 PS Example 1; Fig 1; 52pp; English.
 CC The present sequence is a partial gp41 protein of Human Immunodeficiency
 CC Virus Type 1 (HIV-1) strain BCP13. HIV is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of
 CC antibodies produced in response to HIV infection. BCP13 is a member of
 CC HIV group O (outlier). The present sequence is the immunodominant region
 CC of gp41. This sequence was used in a sequence homology alignment,
 CC which in turn was used to derive a consensus sequence peptide: peptide
 CC 147 (AAB12254).
 CC
 SQ Sequence 33 AA;

Query Match 86.6%; Score 110; DB 21; Length 33;
 Best Local Similarity 90.0%; Pred. No. 1.2e-07;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSGWCCKGRIVCYTSVQNM 20
 |||||
 DB 14 LLSGWCCKGRIVCYTSVQNM 33

RESULT 12

AA05559
 ID AAY05559 standard; Protein; 113 AA.

XX
 AC AAY05559;

XX
 DT 19-JUL-1999 (first entry)

XX
 DE HIV-1 group O isolate BSD189 gp41 antigen.

XX
 XX HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
 vaccine; diagnosis; AIDS.

OS Human immunodeficiency virus type 1.

XX WO9904011-A2.

XX PD 28-JAN-1999.

XX PF 20-JUL-1998; 98WO-EP04522.

XX PR 18-JUL-1997; 97EP-0870110.

XX PA (INNO-) INNOGENETICS NV.

XX PI Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;

XX DR WPI; 1999-132255/11.

XX DR N-PSDB; AAX25167.

PT New isolated HIV-1 group O strains - used to produce
 PT polynucleotides, antigens and antibodies for use in diagnosis and in
 PT vaccines for prevention of HIV-1 infection

PS Claim 3; Fig 6; 162pp; English.

XX

CC The present sequence is an antigen of the gp41 protein of HIV-1
 CC group O (Outlier) strain BSD189, a Cameroon isolate. The
 CC invention relates to new HIV-1 group O antigens (see AAY05546-625),
 CC and the use of these antigens, or nucleic acids encoding them (see
 CC AAX25154-80), in the diagnosis and prophylaxis of AIDS. They can be
 CC used as reagents for detecting HIV-1 group O infection and for
 CC differentiating different types of HIV-1 group O infection.
 CC Vaccines that provide protective immunity against HIV-1 infection, in
 CC particular against HIV-1 group O infection, comprise at least one
 CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a
 CC virus-like particle comprising such an antigen, or an attenuated
 CC form of an HIV-1 type O strain. The invention also relates to new
 CC HIV-1 group O strains, mostly from patients from Cameroon and its
 CC neighbouring countries.
 CC
 SQ Sequence 113 AA;

Query Match 86.6%; Score 110; DB 20; Length 113;
 Best Local Similarity 81.8%; Pred. No. 3.8e-07;
 Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLSGWCCKGRIVCYTSVQNMST 22
 |||||
 DB 39 LLSGWCCKGRIVCYTSVQNMST 60

RESULT 13

AA080460
 ID AAW80460 standard; peptide; 22 AA.

XX
 AC AAW80460;

XX
 DT 28-JAN-1999 (first entry)

XX
 DE Peptide derived from a conserved sequence of group O human HIV.

XX
 KM Group O human immune deficiency virus; HIV; detection; infection.

XX
 OS Synthetic.

XX
 OS Immune deficiency virus.

XX
 PN WO9845323-A1.

XX
 PD 15-OCT-1998.

XX
 PF 06-APR-1998; 98WO-FR00691.

XX
 PR 24-FEB-1998; 98FR-0002212.

XX
 PR 09-APR-1997; 97FR-0004356.

XX
 PA (SNFI) PASTEUR SANOPI DIAGNOSTICS SA.

XX
 PI Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

XX
 DR WPI; 1998-583190/49.

XX
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O

XX
 PS Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).

XX
 SQ Sequence 22 AA;

Query Match 85.8%; Score 109; DB 19; Length 22;
 Best Local Similarity 81.8%; Pred. No. 1.1e-07;
 Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 LLSWGCCKGRILVCTSVQMNST 22
 DB 1 LLSWGCCKGRILVCTSVQMNST 22

RESULT 14

AA012231
 ID AAB12231 standard; peptide; 33 AA.

AC AAB12231;

DT 10-NOV-2000 (first entry)

DE Partial sequence of HIV-1 strain MAN gp41 immunodominant region.

KM HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
 KM acquired immunodeficiency syndrome; group O HIV; gp41; MAN.

XX Human immunodeficiency virus type 1.

XX EPI013766-A2.

XX 28-JUN-2000.

XX 29-NOV-1999; 99EP-0309491.

XX 30-NOV-1998; 98US-0110292.

XX 08-FEB-1999; 99US-0119138.

XX 04-NOV-1999; 99US-0433428.

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX De Leye R. Zheng J;

XX WPI; 2000-402205/35.

XX New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PT virus group O antibodies -

XX Example 1; Fig 1; 52pp; English.

XX The present sequence is a partial gp41 protein of Human Immunodeficiency
 CC Virus Type 1 (HIV-1) strain MAN. HIV is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of
 CC antibodies produced in response to HIV infection. MAN is a member of
 CC HIV group O (outlier). The present sequence is the immunodominant region
 CC of gp41. This sequence was used in a sequence homology alignment,
 CC which in turn was used to derive a consensus sequence peptide: peptide
 CC 147 (AAB12254).

XX Sequence 33 AA;

Query Match 85.8%; Score 109; DB 21; Length 33;
 Best Local Similarity 90.0%; Pred. No. 1.6e-07;

Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCCKGRILVCTSVQMN 20
 DB 14 LLSWGCCKGRILVCTSVQMN 33

RESULT 15

AA007343
 ID AAM07343 standard; peptide; 40 AA.

AC AAM07343;

DT 03-JUN-1997 (first entry)

XX Partial sequence of gp41 from HIV-1 gp. O strain BCF02 (ESS).

XX Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;
 KM C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
 KM primer; hybridisation; amplification; PCR; polymerase chain reaction;
 KM immunogen; antibody.

OS Human immunodeficiency virus type 1.

XX WO9627013-A1.

XX 06-SEP-1996.

XX 26-FEB-1996; 96WO-FR00294.

XX 27-FEB-1995; 95FR-0002236.

PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX ChaiX-Baudier ML, Lousseret-Ajaka I, Ly T, Saragosti S, Simon F;

XX WPI; 1996-412779/41.

XX N-PSDB; AAT44918.

XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 PT immunogens

XX Claim 12; Page 33; 71pp; French.

XX Human immunodeficiency virus type 1 (HIV-1) strains are currently
 CC divided into 2 major groups based on the nucleotide sequences of the
 CC envelop gene (env): group M containing sub-groups A-G, and group O
 CC containing the strains AM70 and MYP5180. The invention relates to the
 CC discovery of several new strains of HIV-1 which can be placed in group O,
 CC based on the partial sequences of the C2V3-env, gp41 and gag genes (see
 CC AAT44907-39 and AAM07329-64). The novel strains have been deposited as
 CC retroviruses CMC1-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07
 CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
 CC presented here is from the strain BCF02 (ESS) and corresponds to a
 CC fragment of the gp41 protein encoded by the env gene. The nucleic acids
 CC can be used to detect gp. O HIV-1 strains by hybridisation or (as
 CC primers) by gene amplification, also for screening and typing of such
 CC strains. Peptides encoded by the nucleic acids can be used as immunogens
 CC to raise Ab for detecting gp. O HIV-1.

XX Sequence 40 AA;

Query Match 85.8%; Score 109; DB 17; Length 40;
 Best Local Similarity 81.8%; Pred. No. 2e-07;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLSWGCCKGRILVCTSVQMNST 22
 DB 19 LLSWGCCKGRILVCTSVQMNWT 40

Search completed: May 29, 2003, 10:36:21
 Job time : 29.3333 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:36 ; Search time 9.95238 Seconds
(without alignments)
65,040 Million cell updates/sec

Title: US-09-147-362a-5

Perfect score: 127
Sequence: 1 LLOGWCKGRVLCYTSVQNMST 22Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	89.8	40	3	US-08-894-699-39
2	114	89.8	40	4	US-09-444-410-39
3	112	88.2	40	3	US-08-894-699-68
4	112	88.2	40	4	US-09-444-410-68
5	111	87.4	41	4	US-08-894-699-67
6	111	87.4	41	4	US-09-444-410-67
7	110	86.6	33	4	US-09-433-428D-6
8	109	85.8	33	4	US-09-433-428D-25
9	109	85.8	40	3	US-08-894-699-36
10	109	85.8	40	3	US-08-894-699-37
11	109	85.8	40	4	US-09-444-410-36
12	109	85.8	40	4	US-09-444-410-37
13	109	85.8	41	4	US-08-894-699-69
14	109	85.8	41	4	US-09-444-410-69
15	107	84.3	33	4	US-09-433-428D-30
16	107	84.3	215	2	US-08-912-129A-58
17	107	84.3	245	2	US-08-912-129A-58
18	107	84.3	373	2	US-08-912-129A-52
19	107	84.3	460	2	US-08-912-129A-60
20	107	84.3	490	2	US-08-912-129A-50
21	107	84.3	618	2	US-08-912-129A-54
22	107	84.3	873	2	US-08-912-129A-61
23	106	83.5	33	4	US-09-433-428D-8
24	106	83.5	40	3	US-08-894-699-40
25	106	83.5	40	4	US-09-444-410-40
26	104	81.9	37	4	US-08-817-441-86
27	104	81.9	40	3	US-08-894-699-41

28	104	81.9	40	3	US-08-894-699-42	Sequence 42, Appl
29	104	81.9	40	4	US-09-444-410-41	Sequence 41, Appl
30	104	81.9	40	4	US-09-444-410-42	Sequence 42, Appl
31	104	81.9	200	4	US-08-965-056-104	Sequence 104, App
32	104	81.9	356	4	US-08-602-713-12	Sequence 12, Appl
33	104	81.9	356	4	US-08-989-493-12	Sequence 12, Appl
34	103	81.1	33	4	US-09-433-428D-4	Sequence 4, Appl
35	103	81.1	33	4	US-09-433-428D-7	Sequence 7, Appl
36	103	81.1	33	4	US-09-433-428D-15	Sequence 15, Appl
37	103	81.1	42	3	US-08-894-699-66	Sequence 66, Appl
38	103	81.1	42	4	US-09-444-410-66	Sequence 66, Appl
39	102	80.3	33	4	US-09-433-428D-5	Sequence 5, Appl
40	102	80.3	33	4	US-09-433-428D-14	Sequence 14, Appl
41	102	80.3	33	4	US-09-433-428D-29	Sequence 29, Appl
42	101	79.5	33	4	US-09-433-428D-10	Sequence 10, Appl
43	101	79.5	33	4	US-09-433-428D-18	Sequence 18, Appl
44	101	79.5	35	4	US-08-817-441-101	Sequence 101, App
45	101	79.5	37	4	US-08-817-441-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-894-699-39
Sequence 39, Application US/08894699

Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P. C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-894-699-39

Query Match 89.8%; Score 114; DB 3; Length 40;
Best Local Similarity 86.4%; Pred. No. 4.7e-10;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQMNST 22
Db 19 LLSWGCKGRIVCYTSVQMNST 40

RESULT 2

US-09-444-410-39
Sequence 39, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/444,410
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-3220
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-39

Query Match 89.8%; Score 114; DB 4; Length 40;
Best Local Similarity 86.4%; Pred. No. 4.7e-10;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQMNST 22
Db 19 LLSWGCKGRIVCYTSVQMNST 40

RESULT 3
US-08-894-699-68
Sequence 68, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-3220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-68

Query Match 88.2%; Score 112; DB 3; Length 40;
Best Local Similarity 86.4%; Pred. No. 9.2e-10;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTSVQMNST 22
Db 19 LLSWGCKGRIVCYTSVQMNST 40

RESULT 4

US-09-444-410-68
Sequence 68, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-3220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-68

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C. SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-68

Query Match 88.2%; Score 112; DB 4; Length 40;
Best Local Similarity 86.4%; Pred. No. 9.2e-10;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTSVQMNST 22
19 LLSWGCKGRIVCYTSVQMNST 40

RESULT 5
US-08-894-699-67
Sequence 67, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-67

Query Match 87.4%; Score 111; DB 3; Length 41;
Best Local Similarity 81.8%; Pred. No. 1.3e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTSVQMNST 22
19 LLSWGCKGRIVCYTSVQMNST 40

RESULT 6
US-09-444-410-67
Sequence 67, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
99-444-410-67

Query Match 87.4%; Score 111; DB 4; Length 41;
Best Local Similarity 81.8%; Pred. No. 1.3e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTYSVQMNST 22
|||
Db 19 LLSWGCKGRIVCTYSVQMNST 40

RESULT 7
US-09-433-428D-6
Sequence 6, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: Zheng, Jian
APPLICANT: De Leye, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: COS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 33
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
09-433-428D-6

Query Match 86.6%; Score 110; DB 4; Length 33;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTYSVQMN 20
|||
Db 14 LLSWGCKGRIVCTYSVQMN 33

RESULT 8
US-09-433-428D-25
Sequence 25, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leye, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: COS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 33

TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-25

Query Match 85.8%; Score 109; DB 4; Length 33;
Best Local Similarity 90.0%; Pred. No. 2.1e-09;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTYSVQMN 20
|||
Db 14 LLSWGCKGRIVCTYSVQMN 33

RESULT 9
US-08-894-699-36
Sequence 36, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEST-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P. C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-36

Query Match 85.8%; Score 109; DB 3; Length 40;
Best Local Similarity 81.8%; Pred. No. 2.5e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCTYSVQMNST 22
|||
Db 19 LLSWGCKGRIVCTYSVQMNST 40

RESULT 10
US-08-894-699-37
Sequence 37, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBION, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-37
Query Match 85.8%; Score 109; DB 3; Length 40;
Best Local Similarity 81.8%; Pred. No. 2.5e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRILVCTSVQNMST 22
DB 19 LLSWGCKGRILVCTSVQNMST 40

RESULT 11
US-09-444-410-36
Sequence 36, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBION, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-36
Query Match 85.8%; Score 109; DB 4; Length 40;
Best Local Similarity 81.8%; Pred. No. 2.5e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRILVCTSVQNMST 22
DB 19 LLSWGCKGRILVCTSVQNMST 40

RESULT 12
US-09-444-410-37
Sequence 37, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA

COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-37

Query Match 85.8%; Score 109; DB 4; Length 40;
Best Local Similarity 81.8%; Pred. No. 2.5e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRLVCYTSVQWNST 22
Db 19 LLSWGCKGRLVCYTSVQWNST 40

RESULT 13
US-08-894-699-69
Sequence 69, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET, FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-69

Query Match 85.8%; Score 109; DB 3; Length 41;
Best Local Similarity 81.8%; Pred. No. 2.6e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRLVCYTSVQWNST 22
Db 19 LLSWGCKGRLVCYTSVQWNST 40

RESULT 14
US-09-444-410-69
Sequence 69, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET, FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-69

Query Match 85.8%; Score 109; DB 4; Length 41;
Best Local Similarity 81.8%; Pred. No. 2.6e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLQSWGCKGRIVCYTSVQWNT 22
Db 19 LLNSWGCKGRQVGYTSVKWNT 40

US-09-433-428D-30
Sequence 30, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 33
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-30

Query Match 84.3%; Score 107; DB 4; Length 33;
Best Local Similarity 85.0%; Pred. No. 4e-09;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLQSWGCKGRIVCYTSVQWNT 20
Db 14 LLNSWGCKGRIVCYTSVKWNT 33

Ch completed: May 29, 2003, 10:41:28
time : 10.9524 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:39:21 ; Search time 19.0317 Seconds
(without alignments)
117.011 Million cell updates/sec

Title: US-09-147-362a-5

Perfect score: 127
Sequence: 1 LLOSMGCKGRLVCTSYKVNST 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

1 number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep:.*
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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep:.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep:.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107	84.3	215	1 US-08-911-824-58	Sequence 58, Appl
2	107	84.3	245	1 US-08-911-824-48	Sequence 48, Appl
3	107	84.3	281	1 US-08-911-824-120	Sequence 120, Appl
4	107	84.3	373	1 US-08-911-824-52	Sequence 52, Appl
5	107	84.3	460	1 US-08-911-824-60	Sequence 60, Appl
6	107	84.3	488	1 US-08-911-824-95	Sequence 95, Appl
7	107	84.3	490	1 US-08-911-824-50	Sequence 97, Appl
8	107	84.3	526	1 US-08-911-824-97	Sequence 97, Appl
9	107	84.3	618	1 US-08-911-824-54	Sequence 93, Appl
10	107	84.3	706	1 US-08-911-824-93	Sequence 91, Appl
11	107	84.3	736	1 US-08-911-824-61	Sequence 86, Appl
12	107	84.3	873	1 US-08-911-824-61	Sequence 86, Appl
13	104	81.9	37	9 US-10-026-741-86	Sequence 104, App
14	104	81.9	200	10 US-09-854-816-104	Sequence 101, Appl
15	101	79.5	35	9 US-10-026-741-101	Sequence 90, Appl
16	101	79.5	37	9 US-10-026-741-7	Sequence 47, Appl
17	101	79.5	37	9 US-10-026-741-90	Sequence 102, App
18	101	79.5	351	9 US-10-026-741-47	
19	101	79.5	877	9 US-10-026-741-102	

20	100	78.7	37	9 US-10-026-741-94	Sequence 94, Appl
21	100	78.7	104	9 US-10-026-741-100	Sequence 100, App
22	99	78.0	37	9 US-10-026-741-88	Sequence 88, Appl
23	97	76.4	35	9 US-09-886-156-62	Sequence 62, Appl
24	97	76.4	35	9 US-09-886-150-62	Sequence 62, Appl
25	97	76.4	35	9 US-09-886-149-62	Sequence 62, Appl
26	97	76.4	35	9 US-09-886-159-62	Sequence 62, Appl
27	97	76.4	146	12 US-10-000-321-10	Sequence 105, App
28	97	76.4	204	10 US-09-854-816-105	Sequence 46, Appl
29	97	76.4	351	9 US-09-886-156-46	Sequence 46, Appl
30	97	76.4	351	9 US-09-886-150-46	Sequence 46, Appl
31	97	76.4	351	9 US-09-886-149-46	Sequence 46, Appl
32	97	76.4	351	9 US-09-886-159-46	Sequence 46, Appl
33	96	75.6	23	9 US-10-026-741-30	Sequence 30, Appl
34	96	75.6	213	10 US-09-854-816-103	Sequence 103, App
35	95	74.8	23	9 US-09-388-847-4	Sequence 84, Appl
36	95	74.8	23	12 US-10-000-321-2	Sequence 2, Appl
37	95	74.8	24	9 US-10-026-741-24	Sequence 34, Appl
38	84	66.1	198	10 US-09-854-816-81	Sequence 81, Appl
39	84	66.1	268	10 US-09-854-816-9	Sequence 9, Appl
40	83	65.4	37	9 US-10-026-741-82	Sequence 82, Appl
41	83	65.4	37	9 US-10-026-741-84	Sequence 84, Appl
42	83	65.4	198	10 US-09-854-816-77	Sequence 77, Appl
43	83	65.4	198	10 US-09-854-816-78	Sequence 78, Appl
44	83	65.4	198	10 US-09-854-816-80	Sequence 80, Appl
45	83	65.4	198	10 US-09-854-816-89	Sequence 89, Appl

ALIGNMENTS

```
RESULT 1
US-08-911-824-58
: Sequence 58, Application US/08911824
: Publication No. US20030004323A1
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
: APPLICANT: Hackett, John R., Jr.
: APPLICANT: Yamaguchi, Julie
: APPLICANT: Goldman, Alan M.
: APPLICANT: Brennan, Catherine A.
: APPLICANT: Hickman, Robert K.
: APPLICANT: Devare, Sushil G.
: TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
: FILE REFERENCE: 6165 US OI
: CURRENT APPLICATION NUMBER: US/08/911,824
: CURRENT FILING DATE: 1997-08-15
: NUMBER OF SEQ ID NOS: 121
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 58
: LENGTH: 215
: TYPE: PRT
: ORGANISM: Human Immunodeficiency Virus
: FEATURE:
: OTHER INFORMATION: Encodes recombinant protein pCO-8PL
US-08-911-824-58
Query Match      84.3%; Score 107; DB 1; Length 215;
Best Local Similarity 77.3%; Pred. No. 5,7e-08;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Cy      1 LLOSMGCKGRLVCTSYKVNST 22
Db      127 LLLNMGCKGRLLCTSYKVNMT 148
RESULT 2
US-08-911-824-48
: Sequence 48, Application US/08911824
: Publication No. US20030004323A1
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
```

```

; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-9PL
US-911-824-48
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Query Match      84.3%; Score 107; DB 1; Length 245;
Best Local Similarity 77.3%; Pred. No. 6.5e-08;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 127 LNLWGCKGRILCTSVKMNST 148
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RESULT 3

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US-08-911-824-120
; Sequence 120, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-15PL
US-08-911-824-120
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Query Match      84.3%; Score 107; DB 1; Length 261;
Best Local Similarity 77.3%; Pred. No. 7.4e-08;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 127 LNLWGCKGRILCTSVKMNST 148
```

RESULT 4

```

US-08-911-824-52
; Sequence 52, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
```

```

; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-11PL
US-08-911-824-52
```

```

Query Match      84.3%; Score 107; DB 1; Length 373;
Best Local Similarity 77.3%; Pred. No. 9.7e-08;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 127 LNLWGCKGRILCTSVKMNST 148
```

RESULT 5

```

US-08-911-824-60
; Sequence 60, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-8CKS
US-08-911-824-60
```

```

Query Match      84.3%; Score 107; DB 1; Length 460;
Best Local Similarity 77.3%; Pred. No. 1.2e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```

Qy 1 LLSWGCKGRIVCTSVQNMST 22
Db 372 LNLWGCKGRILCTSVKMNST 393
```

RESULT 6

```

US-08-911-824-95
; Sequence 95, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
```

```
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 95
LENGTH: 488
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pGO-14PL
US-08-911-824-95
```

```
Query Match      84.3%; Score 107; DB 1; Length 488;
Best Local Similarity 77.3%; Pred. No. 1.2e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1  LLOSNGCKGRIVCYTSVQNMST 22
Db      127 LNLWGCKGRILCYTSVKMNET 148
```

```
RESULT 7
US-08-911-824-50
; Sequence 50, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 490
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pGO-9CKS
US-08-911-824-50
```

```
Query Match      84.3%; Score 107; DB 1; Length 490;
Best Local Similarity 77.3%; Pred. No. 1.3e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1  LLOSNGCKGRIVCYTSVQNMST 22
Db      372 LNLWGCKGRILCYTSVKMNET 393
```

```
RESULT 8
US-08-911-824-97
; Sequence 97, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
```

```
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 97
LENGTH: 526
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pGO-15CKS
US-08-911-824-97
```

```
Query Match      84.3%; Score 107; DB 1; Length 526;
Best Local Similarity 77.3%; Pred. No. 1.3e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1  LLOSNGCKGRIVCYTSVQNMST 22
Db      372 LNLWGCKGRILCYTSVKMNET 393
```

```
RESULT 9
US-08-911-824-54
; Sequence 54, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 618
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pGO-11CKS
US-08-911-824-54
```

```
Query Match      84.3%; Score 107; DB 1; Length 618;
Best Local Similarity 77.3%; Pred. No. 1.6e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1  LLOSNGCKGRIVCYTSVQNMST 22
Db      372 LNLWGCKGRILCYTSVKMNET 393
```

```
RESULT 10
US-08-911-824-93
; Sequence 93, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
```

APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 93
LENGTH: 706
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-13CKS
US-08-911-824-93

Query Match 84.3%; Score 107; DB 1; Length 706;
Best Local Similarity 77.3%; Pred. No. 1.8e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LLSQWCKGRLVCTSVQNMST 22
||| ||||| :||| :|||
DB 618 LNLWCKGRLICYTSVKMNET 639

RESULT 11
US-08-911-824-91
Sequence 91, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 91
LENGTH: 736
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-12CKS
US-08-911-824-91

Query Match 84.3%; Score 107; DB 1; Length 736;
Best Local Similarity 77.3%; Pred. No. 1.8e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LLSQWCKGRLVCTSVQNMST 22
||| ||||| :||| :|||
DB 618 LNLWCKGRLICYTSVKMNET 639

RESULT 12
US-08-911-824-61
Sequence 61, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.

APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 61
LENGTH: 873
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: HIV-1 Group O isolate HAM112
US-08-911-824-61

Query Match 84.3%; Score 107; DB 1; Length 873;
Best Local Similarity 77.3%; Pred. No. 2.2e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LLSQWCKGRLVCTSVQNMST 22
||| ||||| :||| :|||
DB 601 LNLWCKGRLICYTSVKMNET 622

RESULT 13
US-10-026-741-86
Sequence 86, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARBEAU, PIERRE
APPLICANT: CLAVEL, FRANCOISE
APPLICANT: BORMAN, ANDREW
APPLICANT: OUILLENT, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: MONTAGNIER, LUC
APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE
APPLICANT: COHEN, JACQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260, 6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-026-741-86

Query Match 81.9%; Score 104; DB 9; Length 37;
Best Local Similarity 77.3%; Pred. No. 2, 9e-08;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLSGCKGRLVCTSVQNMST 22
14 LLSGCKGRLVCTSVQNMST 35

RESULT 14
9-854-816-104
Sequence 104, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-854-816-104

Query Match 81.9%; Score 104; DB 10; Length 200;
Best Local Similarity 77.3%; Pred. No. 1, 4e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLSGCKGRLVCTSVQNMST 22
14 LLSGCKGRLVCTSVQNMST 22

DB 126 LLSGCKGRLVCTSVQNMST 147

RESULT 15
US-10-026-741-101
Sequence 101, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
OUILLENT, CAROLINE
GUILLET, DENISE
MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQUELINE
COHEN, JACQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegun, Henderson, Farabow, Garrett &
Dunne, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-026-741-101

Query Match 79.5%; Score 101; DB 9; Length 35;
Best Local Similarity 72.7%; Pred. No. 7, 4e-08;
Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLSGCKGRLVCTSVQNMST 22
14 LLSGCKGRLVCTSVQNMST 35

Search completed: May 29, 2003, 11:03:57
Job time: 19.0317 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:06 ; Search time 10.8254 Seconds
(without alignments)
195.370 Million cell updates/sec

Title: US-09-147-362a-5

Sequence: 127
1 LLOSGCKGRLVCTSVQNMST 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues
1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:*

1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	81.9	863	2 A53034	gag polypotein -
2	101	79.5	877	2 S49197	envelope protein p
3	100	78.7	104	2 S52930	Gp41 ENV protein -
4	83	65.4	357	2 S21990	envelope protein g
5	83	65.4	358	2 S22002	envelope protein g
6	83	65.4	443	2 C41621	env polypotein p
7	83	65.4	853	2 S54384	envelope polypote
8	83	65.4	854	1 VCLJST	env polypotein pr
9	83	65.4	855	1 VCLJZR	env polypotein pr
10	82	64.6	358	2 S22000	envelope protein g
11	82	64.6	358	2 S70417	envelope protein g
12	80	63.0	357	2 S22006	envelope protein g
13	80	63.0	357	2 S21994	envelope protein g
14	80	63.0	357	2 S22004	envelope protein g
15	80	63.0	357	2 S21996	envelope protein g
16	80	63.0	357	2 S21992	envelope protein g
17	80	63.0	358	2 S21998	envelope protein g
18	80	63.0	445	2 A41621	env polypotein g
19	80	63.0	454	2 B41621	env polypotein M
20	80	63.0	843	1 H44001	env polypotein D
21	80	63.0	847	2 T09448	env polypotein pr
22	80	63.0	852	2 S13289	env polypotein glycoprot
23	80	63.0	852	1 VCLJBR	env protein - huma
24	80	63.0	852	2 T12016	env polypotein -
25	80	63.0	854	2 S13288	envelope glycoprot
26	80	63.0	855	1 VCLJ28	env protein - huma
27	80	63.0	856	1 VCLJH3	env polypotein pr
28	80	63.0	856	1 VCLJVL	env polypotein pr
29	80	63.0	856	1 VCLJ3W	env polypotein pr

30	80	63.0	856	1 A44963	env polypotein pr
31	80	63.0	859	1 VCLJMN	env polypotein pr
32	80	63.0	861	1 VCLJLV	env polypotein pr
33	80	63.0	861	1 VCLJSC	env polypotein pr
34	80	63.0	868	1 VCLJ4	env polypotein pr
35	79	62.2	846	1 VCLJND	env polypotein pr
36	76	59.8	786	2 S28084	env polypotein -
37	75.5	59.4	151	2 S30448	env protein - huma
38	75.5	59.4	151	2 S30453	env protein - huma
39	75.5	59.4	151	2 S30452	env protein - huma
40	75.5	59.4	151	2 S30450	env protein - huma
41	75.5	59.4	151	2 S30451	env protein - huma
42	74	58.3	729	1 VCLJX	env polypotein pr
43	74	58.3	859	2 T01672	envelope polypote
44	74	58.3	861	1 VCLJKB	env polypotein pr
45	73	57.5	851	2 S33985	env polypotein -

ALIGNMENTS

RESULT 1

A53034
gag polypotein - human immunodeficiency virus type 1 (strain Ant70)

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999

C:Accession: A53034

R:Vanden Haesevelde, M.; Decourt, J.L.; De leys, R.J.; Vandeborgh, B.; van der Groen, J. Virol. 68, 1586-1596, 1994

A:Title: Genomic cloning and complete sequence analysis of a highly divergent African hu

A:Reference number: A53034; MUID:94149849; PMID:8107220

A:Accession: A53034

A:Statut: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-863 <VAN>

A:Cross-references: GB:L02587

C:Superfamily: type B retrovirus env polypotein

C:Keywords: polypotein

Query Match Best Local Similarity 81.9%; Score 104; DB 2; Length 863;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLOSGCKGRLVCTSVQNMST 22
Db 594 LLSLMGCKGRLVCTSVQNMST 615

RESULT 2

S49197
envelope protein precursor - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999

C:Accession: S49197

R:Charneau, P.; Berman, A.M.; Quillent, C.; Guetard, D.; Chameret, S.; Cohen, J.; Remy, J. submitted to the EMBL Data Library, July 1994

A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi

A:Reference number: S49197

A:Accession: S49197

A:Molecule type: DNA

A:Residues: 1-877 <CHA>

A:Cross-references: EMBL:X80020; NID:G510516; PIDN:CA56323.1; PID:G510517

A:Experimental source: isolate VAV

C:Superfamily: type B retrovirus env polypotein

C:Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-535/Product: coat protein gp120 #status predicted <CP1>

F:536-877/Product: coat protein gp41 #status predicted <CP2>

F:698-716/Domain: transmembrane #status predicted <TM>

F:59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,

Query Match Best Local Similarity 79.5%; Score 101; DB 2; Length 877;

Best Local Similarity 72.7%; Pred. No. 1e-06;

Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 LLSQWCKGRILVCYTSVQWNST 22
DB 607 LLLMWCKGRILVCYTSVQWNST 628

RESULT 3

S52930
GP41 ENV protein - human immunodeficiency virus type 1 (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C/Accession: S52930
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
R/Cohen, J.H.M.; Ghetard, D.; Philbert, F.; Chamaret, S.; Tabary, T.; Montagnier, L.; de
submitted to the EMBL Data Library, January 1995
A/Description: A novel HIV-1 O strain illustrates the diversity of the O group.
A/Reference number: S52929
A/Accession: S52930
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-104 <COH>
A/Cross-references: EMBL:X64328; NID:9695526; PIDN:CAA59066.1; PID:9695527
C/Superfamily: type E retrovirus env polyprotein

Query Match 78.7%; Score 100; DB 2; Length 104;
Best Local Similarity 68.2%; Pred. No. 2.2e-07;
Matches 15; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLSQWCKGRILVCYTSVQWNST 22
DB 45 LLLMWCKGRILVCYTSVQWNST 66

RESULT 4

S21990
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 20
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21990; S70423
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A/Reference number: S21990
A/Accession: S21990
A/Molecule type: DNA
A/Residues: 1-357 <STB>
A/Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
R/US Reg. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70423
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-332, 'X', 334-357 <STB2>
A/Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
C/Superfamily: type E retrovirus env polyprotein

Query Match 65.4%; Score 83; DB 2; Length 357;
Best Local Similarity 59.1%; Pred. No. 0.00018;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSQWCKGRILVCYTSVQWNST 22
DB 93 LLLMWCKGRILVCYTSVQWNST 114

RESULT 5

S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 3L

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STB1>
A/Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
R/US Reg. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STB2>
A/Cross-references: EMBL:X61352; NID:960186
C/Superfamily: type E retrovirus env polyprotein

Query Match 65.4%; Score 83; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00018;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSQWCKGRILVCYTSVQWNST 22
DB 94 LLLMWCKGRILVCYTSVQWNST 115

RESULT 6

C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N/Alternate names: coat polyprotein
N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C/Accession: C41621
R/Burger, H.; Welsch, B.; Flaherty, K.; Guille, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A/Reference number: M1621; MUID:92107924; PMID:1765038
A/Accession: C41621
A/Molecule type: DNA
A/Residues: 1-443 <BUR>
A/Cross-references: GB:M77230; NID:9328631; PIDN:AA803792.1; PID:9555015
A/Note: this virus was isolated from the mother's sexual partner
C/Genetics:

A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/DNA: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,365,365,377/Binding site: ca

Query Match 65.4%; Score 83; DB 2; Length 443;
Best Local Similarity 59.1%; Pred. No. 0.00022;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSQWCKGRILVCYTSVQWNST 22
DB 332 LLLMWCKGRILVCYTSVQWNST 353

RESULT 7

S54384
envelope polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C/Accession: S54384
R/Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <THE>
A:Cross-references: EMBL:M22619; NID:g329377; PIDN:AAA45370.1; PID:g329385
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: polyprotein

Query Match 65.4%; Score 83; DB 2; Length 853;
Best Local Similarity 59.1%; Pred. No. 0.00039;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRIVCYTSVQMNST 22
DB 589 LIGWCGSGKLICTTVPWNNS 610

RESULT 8

polyprotein precursor - simian immunodeficiency virus SIVcpz
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: simian immunodeficiency virus SIVcpz

A:Note: host Pan troglodytes (chimpanzee)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
A:Accession: S05990
R:Huet, T.; Cheynier, R.; Meyers, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Reference number: S05983; MUID:90259077; PMID:2188136
A:Accession: S05990
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-854 <HUS>

A:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36407.1; PID:g58874
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-500/Product: coat protein gp120 #status predicted <CP1>
F:501-854/Product: coat protein gp41 #status predicted <CP2>
F:501-517/Domain: transmembrane #status predicted <TM1>
F:675-693/Domain: transmembrane #status predicted <TM2>
F:805-821/Domain: transmembrane #status predicted <TM3>
F:134,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 65.4%; Score 83; DB 1; Length 854;
Best Local Similarity 54.5%; Pred. No. 0.00039;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRIVCYTSVQMNST 22
DB 582 LIGWCGSGKAVCTTVPWNNS 603

RESULT 9

env polyprotein precursor - human immunodeficiency virus Zr-6
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus Zr-6
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
A:Accession: D26192

R:Srivivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot
A:Reference number: A26192; MUID:8748097; PMID:3036660
A:Accession: D26192
A:Molecule type: DNA
A:Residues: 1-855 <SRI>

A:Cross-references: GB:X03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403

C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polyprotein #status predicted <MAT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 65.4%; Score 83; DB 1; Length 855;
Best Local Similarity 59.1%; Pred. No. 0.00039;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRIVCYTSVQMNST 22
DB 591 LIGWCGSGKLICTTVPWNNS 612

RESULT 10

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
A:Accession: S22000
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as deter
A:Reference number: S21990
A:Accession: S22000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polyprotein

Query Match 64.6%; Score 82; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00025;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRIVCYTSVQMNST 22
DB 94 LIGWCGSGKRLCTTVPWNNS 115

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
A:Accession: S70417

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA43614.1; PID:g60185
C:Superfamily: type E retrovirus env polyprotein

Query Match 64.6%; Score 82; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00025;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRIVCYTSVQMNST 22
DB 94 LIGWCGSGKRLCTTVPWNNS 115

RESULT 12

A: Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by a difference number 00000

Job time : 10.8254 secs

Search completed: May 29, 2003, 10:40:24
Job time : 10.8254 secs


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FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 853 AA; 97043 MW; 849808BCBAF7008 CRC64;

Query Match 65.4%; Score 83; DB 1; Length 853;
Best Local Similarity 59.1%; Pred. No. 3.5e-05;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LQSGGCKGRVLCYTSVQNMST 22
Db 589 ILGLMGSGKRLICTTVPMNSS 610

RESULT 2
ENV_SIVCZ STANDARD; PRT; 854 AA.
AC P17281;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90259077; PubMed=2188136;
Huet T., Cheyrier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
-!- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPROTEIN.
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DR EMBL, X52154; CAA36407.1; -
DR PIR, S09990; VCLJ51.
DR HIV, X52154; ENVSCPZ.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam, PF00516; GP120.1.
DR Pfam, PF00517; GP41.1.
DR AIDS, Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KM Signal.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 31 500 TRANSMEMBRANE GLYCOPROTEIN.
FT CHAIN 501 854 POTENTIAL.
FT TRANSMEM 501 517

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FT TRANSMEM 675 693 POTENTIAL.
FT TRANSMEM 805 821 POTENTIAL.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 854 AA; 95803 MW; 2E249AFAD4F2D9B3 CRC64;

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Query Match 65.4%; Score 83; DB 1; Length 854;
Best Local Similarity 54.5%; Pred. No. 3.6e-05;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Oy 1 LQSGGCKGRVLCYTSVQNMST 22
Db 582 ILGLMGSGKRAVCYTVPMNSS 603

RESULT 3
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
Strinivasan A., Anand R., York D., Ranganathan P., Porino P.,
Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
Sánchez-Pescador R.;
"Molecular characterization of human immunodeficiency virus from
RT Zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene.";
Gene 52:71-82(1987).
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CC -----
DR EMBL, K03458; AAA45380.1; -
DR PIR, D26192; VCLJ2R.

```

DR HIV: K03458; ENV526.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 510
FT CHAIN 511 855
FT DISULFID 53 73
FT DISULFID 118 207
FT DISULFID 125 198
FT DISULFID 130 155
FT DISULFID 220 249
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FT CARBOHYD 673 673
SQ SEQUENCE 855 AA; 96971 MW; 384D3D6E239C3457 CRC64;
Query Match 65.4%; Score 83; DB 1; Length 855;
Best Local Similarity 59.1%; Pred. No. 3.6e-05;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Cy 1 LIGSGCKGRVLYCYTVQNMST 22
Db 591 LIGSGCKGRVLYCYTVQNMST 612
ENV_HV12 STANDARD; PRT; 843 AA.
AC P35961;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).

OC Viruses; Retrovirus; Retroviridae; Lentivirus.
OX NCBI TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation.";
RU J. Virol. 66:6587-6600(1992).
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CC EMBL: M93258; -; NOT_ANNOTATED_CDS.
CC PIR: H44001; H44001.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 489
FT CHAIN 490 843
FT TRANSMEM 738 755
FT DISULFID 53 73
FT DISULFID 118 201
FT DISULFID 125 192
FT DISULFID 130 155
FT DISULFID 214 243
FT DISULFID 224 235
FT DISULFID 292 326
FT DISULFID 373 432
FT DISULFID 380 405
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 138 138
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 193 193
FT CARBOHYD 230 230
FT CARBOHYD 237 237
FT CARBOHYD 258 258
FT CARBOHYD 272 272
FT CARBOHYD 285 285
FT CARBOHYD 291 291
FT CARBOHYD 297 297
FT CARBOHYD 327 327
FT CARBOHYD 351 351
FT CARBOHYD 381 381
FT CARBOHYD 389 389
FT CARBOHYD 395 395
FT CARBOHYD 400 400
FT CARBOHYD 435 435
FT CARBOHYD 450 450
FT CARBOHYD 598 598
FT CARBOHYD 603 603
FT CARBOHYD 612 612
FT CARBOHYD 624 624
FT CARBOHYD 803 803
SQ SEQUENCE 843 AA; 95648 MW; C69DPD971C918B71 CRC64;
Query Match 63.0%; Score 80; DB 1; Length 843;
Best Local Similarity 54.5%; Pred. No. 0.0001;

[illegible][illegible]

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FT CARBOHD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 852 AA; 9663 MW; E7BF8D23C9910D CRC64;

Query Match 63.0%; Score 80; DB 1; Length 852;
Best Local Similarity 54.5%; Pred. No. 0.0001;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 LLSQWCKGRVLYCYTSVQMNST 22
588 LLSQWCKGRVLYCYTSVQMNST 609

RESULT 10
ENV_HV1MF STANDARD; PRT; 853 AA.
AC P19551;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C.,
RA Maslak A.;
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis."
RL J. Virol. 64:3792-3803(1990).
CC -----
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CC -----
CC EMBL; M33943; AAA44850.1; -
CC DR HIV; M33943; ENVSMFA.
CC DR InterPro: IPR000328; Env GP41.
CC DR InterPro: IPR000777; GP120.
CC DR Pfam: PF00516; GP120; 1.
CC DR Pfam: PF00517; GP41; 1.
CC DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
CC signal.
CC KM SIGNAL.
FT CHAIN 1 30
FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFD 54 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFD 119 74 BY SIMILARITY.
FT DISULFD 126 194 BY SIMILARITY.
FT DISULFD 131 157 BY SIMILARITY.
FT DISULFD 216 245 BY SIMILARITY.
FT DISULFD 226 237 BY SIMILARITY.
FT DISULFD 294 329 BY SIMILARITY.
FT DISULFD 376 443 BY SIMILARITY.

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FT DISULFD 383 416 BY SIMILARITY.
FT CARBOHD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 853 AA; 96912 MW; 337B93B6F22ABA CRC64;

Query Match 63.0%; Score 80; DB 1; Length 853;
Best Local Similarity 54.5%; Pred. No. 0.0001;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 LLSQWCKGRVLYCYTSVQMNST 22
590 LLSQWCKGRVLYCYTSVQMNST 611

RESULT 11
ENV_HV1A2 STANDARD; PRT; 855 AA.
AC P03378;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV/SF2 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempien M.W., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2)."
RL Science 227:484-492(1985).
CC -----
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CC -----
CC EMBL; X02007; AAB59882.1; -

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DR PIR: A03976; VCLJ2.
DR HIV: K02007; ENV5SF2.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00516; GP120.
DR Pfam: PF00517; GP41.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 208
FT DISULFID 125 159
FT DISULFID 130 155
FT DISULFID 221 250
FT DISULFID 231 242
FT DISULFID 239 333
FT DISULFID 360 442
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FT CARBOHYD 154 154
FT CARBOHYD 158 158
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FT CARBOHYD 190 190
FT CARBOHYD 200 200
FT CARBOHYD 203 233
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FT CARBOHYD 815 815
SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC1A2 CR664;

Query Match 63.0%; Score 80; DB 1; Length 855;
Best Local Similarity 54.5%; Pred. No. 0.0001;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LIGSWGCGRLVCTYSVOMNST 22
Db 591 LIGWCGSKLCTTAVPNMAS 612

RESULT 12
ENV_HVIOY STANDARD; PRT; 855 AA.
AC P20888;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).

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CC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11699;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90148544; PubMed=2559749;
RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
individual presenting an atypical western blot.";
RL Aids 3:707-715 (1989).
CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
HEALTHY GABONESE INDIVIDUAL.
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CC EMBL: M26727; AAA83397.1; -.
DR HIV: M26727; ENV5OY1.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.
DR Pfam: PF00517; GP41.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
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FT CARBOHYD 815 815
SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CR664;

Query Match 63.0%; Score 80; DB 1; Length 855;
Best Local Similarity 54.5%; Pred. No. 0.0001;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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ID	ENV	HV1B1	STANDARD;	PRT;	856 AA.
AC	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
EN	ENV.				
OS	Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).				
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirinae.				
OX	NCBI_TaxID=11678;				
RA	SEQUENCE FROM N.A.				
RA	MEDLINE=85111123; PubMed=2578615;				
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Chayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;				
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.",				
RL	Nature 313:277-284(1985).				
RL	[2]				
RP	DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.				
RP	MEDLINE=90285159; PubMed=235506;				
RA	Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N., Gregory T.J.;				
RA	"Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in Chinese hamster ovary cells."				
RL	J. Biol. Chem. 265:10373-10382(1990).				
CC	-----				
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CC	-----				
DR	EMBL, M15654; AAA44205.1; -				
PIR	A03973; VCLJH3.				
DR	HIV, M15654; ENV5BH102.				
DR	InterPro; IPR000328; Env GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120; 1.				
DR	Pfam; PF00517; GP41; 1.				
KM	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.				
KM	SIGNAL				
FT	CHAIN	1	30		
FT	CHAIN	511	511		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	512	856		TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74		
FT	DISULFID	119	205		
FT	DISULFID	126	196		
FT	DISULFID	131	157		
FT	DISULFID	218	247		
FT	DISULFID	228	239		
FT	DISULFID	226	331		
FT	DISULFID	378	445		
FT	DISULFID	385	418		
FT	CARBOHYD	88	88		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	136	136		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	141	141		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	156	156		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	160	160		N-LINKED (GLCNAC. . .)

[illegible]

Query Match	Similarity	54.5%	Score 80	DB 1	Length 856
Best Local	Similarity	54.5%	Pred. No.	0.0001	
Matches	12	Conservative	5	Mismatches	5
				Indels	0
				Gaps	0
QY	1	LLQSGCKGRLLVCYTSYQMNST	22		
DB	592	LLGIWCGSGKILCTTAVPNNAS	613		

Search completed: May 29, 2003, 10:36:59
Job time : 6.4127 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:32:35 ; Search time 22.6984 Seconds
(without alignments)
199.707 Million cell updates/sec

Title: US-09-147-362a-5
Perfect score: 127
Sequence: 1 LLSWGCKGRLLVCYTSVQNMST 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	90.6	219	15 Q91EB6	Q91eb6 human immun
2	114	89.8	135	15 Q9DOL9	Q9dql9 human immun
3	114	89.8	216	15 Q91EC5	Q91ec5 human immun
4	114	89.8	242	15 Q91E31	Q91e31 human immun
5	112	88.2	214	15 Q9D1K3	Q9d1k3 human immun
6	111	87.4	116	15 Q11941	Q11941 human immun
7	111	87.4	116	15 Q40458	Q40458 human immun
8	111	87.4	130	15 Q91HU9	Q91hu9 human immun
9	111	87.4	183	15 Q91EC1	Q91ec1 human immun
10	111	87.4	218	15 Q91E95	Q91e95 human immun
11	111	87.4	220	15 Q91EC9	Q91ec9 human immun
12	111	87.4	512	15 Q91ED2	Q91ed2 human immun
13	111	87.4	538	15 Q91ED5	Q91ed5 human immun
14	111	87.4	872	15 Q807H0	Q8q7h0 human immun
15	111	87.4	879	15 Q9W1U9	Q9w1u9 human immun
16	111	87.4	880	15 Q807I9	Q8q7i9 human immun

17	111	87.4	882	15 Q807F9	Q8q7f9 human immun
18	111	87.4	887	15 Q807H6	Q8q7h6 human immun
19	111	87.4	887	15 Q807G9	Q8q7g9 human immun
20	111	87.4	900	15 Q9QN28	Q9qn28 human immun
21	110	86.6	114	15 Q40448	Q40448 human immun
22	110	86.6	235	15 Q91E54	Q91e54 human immun
23	109	85.8	118	15 Q40451	Q40451 human immun
24	109	85.8	214	15 Q91E96	Q91e96 human immun
25	109	85.8	216	15 Q91EC7	Q91ec7 human immun
26	109	85.8	216	15 Q91EA5	Q91ea5 human immun
27	109	85.8	219	15 Q91EC8	Q91ec8 human immun
28	109	85.8	234	15 Q91EA6	Q91ea6 human immun
29	109	85.8	242	15 Q91E30	Q91e30 human immun
30	109	85.8	535	15 Q91EF2	Q91ef2 human immun
31	109	85.8	544	15 Q91ED9	Q91ed9 human immun
32	109	85.8	548	15 Q91ED6	Q91ed6 human immun
33	109	85.8	551	15 Q91EB1	Q91eb1 human immun
34	109	85.8	865	15 Q807H7	Q8q7h7 human immun
35	109	85.8	867	15 Q807G8	Q8q7g8 human immun
36	108	85.0	116	15 Q40459	Q40459 human immun
37	108	85.0	134	15 Q91HV4	Q91hv4 human immun
38	108	85.0	137	15 Q91HV5	Q91hv5 human immun
39	108	85.0	146	15 Q9WRV2	Q9wrv2 human immun
40	108	85.0	200	15 Q91E88	Q91e88 human immun
41	108	85.0	227	15 Q91E99	Q91e99 human immun
42	108	85.0	238	15 Q91DK1	Q91dk1 human immun
43	108	85.0	517	15 Q91EB7	Q91eb7 human immun
44	108	85.0	875	15 Q807H4	Q8q7h4 human immun
45	107	84.3	114	15 Q40457	Q40457 human immun

ALIGNMENTS

RESULT 1									
ID	Q91EB6	PRELIMINARY;	PRT;	219 AA.					
AC	Q91EB6;								
DR	01-OCT-2000 (TREMBLrel. 15, Created)								
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)								
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)								
DE	Gp41 (Fragment).								
CN	ENV.								
OS	Human immunodeficiency virus type 1.								
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.								
OX	NCBI_TaxID=11676;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=BCF14;								
RA	Roques P., Robertson D., Sandrine S., Christel D., Francois S.,								
RA	Philippe M.;								
RT	"Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."								
RL	Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.								
DR	EMBL; AJ236404; CAB96252.1; -								
DR	InterPro; IPR000328; Env_GP41.								
DR	Pfam; PF00517; GP41; 1.								
KW	Transmembrane.								
FT	NON_TER	1	219	1					
FT	NON_TER	219	219	1					
SO	SEQUENCE	219 AA;	25353 MW;	F65829EB01520D91 CRC64;					
Query Match									
Best Local Similarity 90.6%; Score 115; DB 15; Length 219;									
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;									
QY	1	LLSWGCKGRLLVCYTSVQNMST	22						
DB	57	LLSWGCKGRLLVCYTSVQNMST	78						
RESULT 2									
ID	Q9DOL9	PRELIMINARY;	PRT;	135 AA.					

AC 09DOL9;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP-M1321;
RX MEDLINE=20584646; Pubmed=11153079;
RA Ortiz M., Munoz L., Bernal A., Rodriguez A., Zorrano A.,
RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."
RL Molecular Characterization of Non-B HIV Type 1 Subtypes from Africa
in Spain."
DR AIDS Res. Hum. Retroviruses 16:1967-1971(2000).
EMBL; AF255939; AAC36894.1; -
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 135
SQ SEQUENCE 135 AA; 16285 MW; D34B9EF77318B36 CRC64;

Query Match 89.8%; Score 114; DB 15; Length 135;
Best Local Similarity 81.8%; Pred. No. 2e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLOSMGCKRLVCTSVQNMST 22
DB 48 LLSWGCKRGRLCYTSVKMNST 69

RESULT 3
O9IECS PRELIMINARY; PRT; 216 AA.
AC O9IECS;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF07;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ236394; CAB96243.1; -
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 25027 MW; 413AE9BBF1B4FC9A CRC64;

Query Match 89.8%; Score 114; DB 15; Length 216;
Best Local Similarity 86.4%; Pred. No. 3.2e-10;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLOSMGCKRLVCTSVQNMST 22
DB 47 LLSWGCKRGRLCYTSVKMNST 68

ID O9IE31 PRELIMINARY; PRT; 242 AA.
AC O9IE31;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE TM, GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF112;
RA Roques P., Robertson D., Souquiere S., Diamond F., Mauciere P.,
RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ243366; CAB96336.1; -
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 242
SQ SEQUENCE 242 AA; 27539 MW; DE8A73DF0E8A6FD7 CRC64;

Query Match 89.8%; Score 114; DB 15; Length 242;
Best Local Similarity 81.8%; Pred. No. 3.6e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLOSMGCKRLVCTSVQNMST 22
DB 64 LLSWGCKRGRLCYTSVKMNST 85

RESULT 5
O9DIK3 PRELIMINARY; PRT; 214 AA.
AC O9DIK3;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE GP41 protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF120;
RA Roques P., Robertson D., Diamond F., Souquiere S., Mauciere P.,
RT "Phylogenetic analysis of 49 newly derived HIV-1 group O strains: High
RT viral diversity but no group M-like subtypes."
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ298125; CAC18806.1; -
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 24436 MW; FFAB90D08F61ABB CRC64;

Query Match 88.2%; Score 112; DB 15; Length 214;
Best Local Similarity 81.8%; Pred. No. 6.6e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLOSMGCKRLVCTSVQNMST 22
DB 45 LLSWGCKRGRLCYTSVKMNST 66

RESULT 4
O9IE31

RESULT 6
O11941

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ID 011941 PRELIMINARY; PRT; 116 AA.
AC 011941;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
ENvelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB1124;
RX MEDLINE=97340911; PubMed=9197385;
RA Brennan C.A., Hackett J. Jr., Zekeng L., Lund J.K., Vallari A.S.,
RA Hickman R.K., Gurtler L., Kapure L., von Overbeck J., Hampel H.,
RA Devere S.G.;
RT "Sequence of gp120env immunodominant region of HIV type 1 group O from
RT west central Africa."
RT AIDS Res. Hum. Retroviruses 13:901-904(1997).
DR EMBL; U90134; AAB62817.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 13789 MW; 4889A940F4255E3E CRC64;

Query Match 87.4%; Score 111; DB 15; Length 116;
Best Local Similarity 81.8%; Pred. No. 5.1e-10;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLOSWGCKGRILVCTSVQNMST 22
DB 39 LNLWCKGRILVCTSVQNMST 60

RESULT 7
ID 040458 PRELIMINARY; PRT; 116 AA.
AC 040458;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
ENvelope transmembrane glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GROUP O;
RA Bibollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;
RT "Molecular characterization of envelope transmembrane glycoprotein of
RT 14 new human immunodeficiency virus type 1 group O strains from
RT different African countries."
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y09774; CAAT0913.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 13865 MW; 540F5B3B7AD849D8 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 116;
Best Local Similarity 81.8%; Pred. No. 5.1e-10;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLOSWGCKGRILVCTSVQNMST 22
DB 39 LNLWCKGRILVCTSVQNMST 60
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RESULT 8
ID 091H09 PRELIMINARY; PRT; 130 AA.
AC 091H09;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
ENvelope glycoprotein (Fragment).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CM798;
RX MEDLINE=20386754; PubMed=10933623;
RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O."
RT AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229235; AAF71912.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15593 MW; 5385789A36344EA CRC64;

Query Match 87.4%; Score 111; DB 15; Length 130;
Best Local Similarity 81.8%; Pred. No. 5.8e-10;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLOSWGCKGRILVCTSVQNMST 22
DB 40 LNLWCKGRILVCTSVQNMST 61

RESULT 9
ID 091EC1 PRELIMINARY; PRT; 183 AA.
AC 091EC1;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCE101;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ236398; CAB96247.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1
FT NON_TER 183
SQ SEQUENCE 183 AA; 21722 MW; C22A28A73540C8AA CRC64;

Query Match 87.4%; Score 111; DB 15; Length 183;
Best Local Similarity 81.8%; Pred. No. 8.1e-10;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLOSWGCKGRILVCTSVQNMST 22
DB 42 LNLWCKGRILVCTSVQNMST 63
```

RESULT 10

Q9IE95 ID Q9IE95 PRELIMINARY; PRT; 218 AA.
AC Q9IE95; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF51;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S., Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
EMBL AJ236425; CAB96273.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 218 AA; 25243 MW; E7F0E1E20EF79FA8 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 218;
Best Local Similarity 77.3%; Pred. No. 9.7e-10;

Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRILVCTSVQNMST 22
DB 54 LLSWGCKGRILVCTSVQNMST 75

RESULT 11

Q9IEC9 ID Q9IEC9 PRELIMINARY; PRT; 220 AA.
AC Q9IEC9; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF01;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S., Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
EMBL AJ236390; CAB96239.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 220 AA; 25503 MW; 8D67EAC48DD40BD1 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 220;
Best Local Similarity 81.8%; Pred. No. 9.8e-10;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRILVCTSVQNMST 22
DB 53 LLSWGCKGRILVCTSVQNMST 74

RESULT 12

Q9IED2 ID Q9IED2 PRELIMINARY; PRT; 512 AA.
AC Q9IED2; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF101;
RA Roques P., Robertson D., Diamond F., Souquiere S., Mauciere P., Deleigne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."
Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
EMBL AJ133075; CAB96236.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 512 AA; 57977 MW; 4FF658B2C15CE492 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 512;
Best Local Similarity 81.8%; Pred. No. 2.3e-09;

Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRILVCTSVQNMST 22
DB 372 LLSWGCKGRILVCTSVQNMST 393

RESULT 13

Q9IED5 ID Q9IED5 PRELIMINARY; PRT; 538 AA.
AC Q9IED5; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF51;
RA Roques P., Robertson D., Diamond F., Souquiere S., Mauciere P., Deleigne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."
Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
EMBL AJ133072; CAB96233.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 538 AA; 60777 MW; B3C9E6A233FEF1D CRC64;

Query Match 87.4%; Score 111; DB 15; Length 538;
Best Local Similarity 77.3%; Pred. No. 2.4e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLOSNGCKGRILVCTSVQNMST 22
DB 53 LLSWGCKGRILVCTSVQNMST 74

Db 374 LLSWGCKGRLCYTSVQNMNTT 395

RESULT 14

0807H0 PRELIMINARY; PRT; 872 AA.

ID 0807H0

AC 0807H0; 01-JUN-2002 (TRENBLrel. 21, Created)

DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DE Envelope glycoprotein.

ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=98CMA453;

RX MEDLINE=21849375; PubMed=11860674;

RY Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kapane L., Ngansop C., Zekeng L., Gurtler L.G., Devare S.G., Brennan C.A.; "Evaluation of HIV Type 1 Group O Isolates: Identification of Five Phylogenetic Clusters";

RT AIDS Res. Hum. Retroviruses 18:269-282 (2002).

RL EMBL; AF383251; AAL98873.1;

SQ SEQUENCE 872 AA; 98344 MW; 91D37F60053827E3 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 872;

Best Local Similarity 81.8%; Pred. No. 3.9e-09;

Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLCYTSVQNMNTT 22

DB 602 LLSWGCKGRLCYTSVQNMNTT 623

RESULT 15

Q9WIU9 PRELIMINARY; PRT; 879 AA.

AC Q9WIU9;

DT 01-NOV-1999 (TRENBLrel. 12, Created)

DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)

DE Gp160 precursor.

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VI686;

RX MEDLINE=99223950; PubMed=10207543;

RY Janssens W., Heyndrickx L., Van der Auwera G., Nkengasong J., Beilnaert E., Vereecken K., Coppens S., Willems B., Franssen K., Peeters M., Ndumbe P., Delaporte E., Van der Groen G.; "Interpatient genetic variability of HIV-1 group O.";

RT AIDS 13:41-48 (1999).

RL [12]

RP SEQUENCE FROM N.A.

RC STRAIN=VI686;

RX MEDLINE=96426454; PubMed=828748;

RY Delaporte E., Janssens W., Peeters M., Buve A., Dibanga G., Perret J.L., Ditsambou V., Georges Courbot M.C., Georges A., Bourgeois A., Samb B., Henzel D., Heyndrickx L., Franssen K., Van der Groen G., Larouz B., Mbe J.R.; "Epidemiological and Molecular characteristics of HIV infection in Gabon (1986 - 1994).";

RT AIDS 10:903-910 (1996).

RL EMBL; X96526; CAA65373.1;

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120, 1.

DR Pfam; PF00517; GP41, 1.

KM AIDS, Coat protein; Glycoprotein; Polypeptide; Signal; Transmembrane.

FT SIGNAL 1 29

FT CHAIN 30 524 GP120.

FT CHAIN 132 156 V1.

FT CHAIN 164 200 V2.

FT CHAIN 302 335 V3.

FT CHAIN 395 427 V4.

FT CHAIN 458 475 V5.

FT CHAIN 525 879

SQ SEQUENCE 879 AA; 99099 MW; BC6422ADDFA3409 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 879;

Best Local Similarity 81.8%; Pred. No. 4e-09;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLCYTSVQNMNTT 22

DB 605 LLSWGCKGRLCYTSVQNMNTT 626

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20 ; Search time 29.3333 Seconds
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99.938 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	127	100.0	22	19	AAW80466
2	124	97.6	22	19	AAW80461
3	121	95.3	22	19	AAW80460
4	120	94.5	32	19	AAW80469
5	119	93.7	22	19	AAW80462
6	117	92.1	40	17	AAW07346
7	116	91.3	22	19	AAW80464
8	115	90.6	22	19	AAW80465
9	115	90.6	22	19	AAW80463
10	114	89.8	32	19	AAW80470

11	113	89.0	22	19	AAW80459	Peptide derived fr
12	113	89.0	32	19	AAW80471	Peptide derived fr
13	110	86.6	40	17	AAW07352	Partial sequence O
14	110	86.6	113	20	AAW05565	HIV-1 group O isol
15	110	86.6	200	21	AAW77373	HIV-1 group O env
16	110	86.6	215	20	AAW09499	HIV-1 group O env
17	110	86.6	215	20	AAW06983	Recombinant pCO-8P
18	110	86.6	215	21	AAW77374	HIV-1 group O env
19	110	86.6	245	20	AAW09493	HIV-1 group O env
20	110	86.6	245	20	AAW06977	Recombinant pCO-9P
21	110	86.6	245	21	AAW77369	HIV-1 group O pCO-
22	110	86.6	281	20	AAW09507	HIV-1 group O env
23	110	86.6	373	20	AAW09495	HIV-1 group O env
24	110	86.6	373	20	AAW06979	Recombinant pCO-11
25	110	86.6	460	20	AAW09500	HIV-1 group O env
26	110	86.6	460	20	AAW06984	Recombinant pCO-8C
27	110	86.6	460	21	AAW77375	HIV-1 group O env
28	110	86.6	474	21	AAW77371	HIV-1 group O env
29	110	86.6	488	20	AAW09504	HIV-1 group M and
30	110	86.6	490	20	AAW09494	HIV-1 group O env
31	110	86.6	490	20	AAW06978	Recombinant pCO-9C
32	110	86.6	490	21	AAW77370	HIV-1 group O env
33	110	86.6	526	20	AAW09505	HIV-1 group O poly
34	110	86.6	618	20	AAW09496	HIV-1 group O env
35	110	86.6	618	20	AAW06980	Recombinant pCO-11
36	110	86.6	618	21	AAW77372	HIV-1 group O env
37	110	86.6	706	20	AAW09503	HIV-1 group M and
38	110	86.6	715	20	AAW05625	HIV-1 group O isol
39	110	86.6	736	20	AAW09502	HIV-1 group M and
40	110	86.6	873	20	AAW09501	HIV-1 group O env
41	110	86.6	873	20	AAW06985	Amino acid sequenc
42	110	86.6	873	21	AAW77376	HIV-1 group O isol
43	109	85.8	104	17	AAW07245	HIV-1 group O extra
44	108	85.0	33	21	AAW12212	Partial sequence O
45	107	84.3	33	21	AAW12231	Partial sequence O

ALIGNMENTS

RESULT 1
AAW80466
ID AAW80466 standard; peptide; 22 AA.
AC AAW80466;
DT 28-JAN-1999 (first entry)
XX Peptide derived from a conserved sequence of group O human HIV.
DB Peptide derived from a conserved sequence of group O human HIV.
KW Group O human immune deficiency virus; HIV; detection; infection.
OS Synthetic.
OS Immune deficiency virus.
PN WO9845323-A1.
PD 15-OCT-1998.
XX
PF 06-APR-1998; 98WO-FR00691.
XX
PR 24-FEB-1998; 98FR-0002212.
PR 09-APR-1997; 97FR-0004356.
XX
PA (SNFI) PASTEUR SANOPT DIAGNOSTICS SA.
XX
PI Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY.
XX WPI; 1998-583190/49.
DR
XX
PT New synthetic peptide(s) - useful for, e.g. detecting infection by
PT human immune deficiency virus of group O
XX

PS Claim 6; Page 43; 55pp; French.

XX AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 100.0%; Score 127; DB 19; Length 22;
Best Local Similarity 100.0%; Pred. No. 9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCRGRLVCTYSVQNMET 22
DB 1 LLSWGCRGRLVCTYSVQNMET 22

PLT 2
AAW80461

ID AAW80461 standard; peptide; 22 AA.

AC AAW80461;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KW Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PA Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

PI WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by

PT human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 97.6%; Score 124; DB 19; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.2e-09;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCRGRLVCTYSVQNMET 22
DB 1 LLSWGCRGRLVCTYSVQNMET 22

RESULT 3

AAW80460

ID AAW80460 standard; peptide; 22 AA.

AC AAW80460;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KW Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PA Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

PI WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by

PT human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 95.3%; Score 121; DB 19; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.3e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCRGRLVCTYSVQNMET 22
DB 1 LLSWGCRGRLVCTYSVQNMET 22

RESULT 4

AAW80469

ID AAW80469 standard; peptide; 32 AA.

AC AAW80469;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KW Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

PN WO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

XX 24-FEB-1998; 98FR-0002212.
 PR 09-APR-1997; 97FR-0004356.
 XX
 PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 XX Chenebaux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;
 XX WPI; 1998-583190/49.
 DR
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX
 PS Claim 6; Page 44; 55pp; French.
 XX
 CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SO Sequence 32 AA;
 Query Match 94.5%; Score 120; DB 19; Length 32;
 Best Local Similarity 90.9%; Pred. No. 1e-08;
 Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLSWGCGRLVCTYSVQNMET 22
 DB 11 LLSWGCGRLVCTYSVQNMET 32
 RESULT 5
 AAW80462
 ID AAW80462 standard; peptide; 22 AA.
 AC AAW80462;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Peptide derived from a conserved sequence of group O human HIV.
 XX
 KW Group O human immune deficiency virus; HIV; detection; infection.
 XX
 OS Synthetic.
 OS Immune deficiency virus.
 OS
 WO9845323-A1.
 PD 15-OCT-1998.
 XX
 PF 06-APR-1998; 98WO-FR00691.
 XX
 PR 24-FEB-1998; 98FR-0002212.
 PR 09-APR-1997; 97FR-0004356.
 XX
 PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 PI Chenebaux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;
 DR WPI; 1998-583190/49.
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX
 PS Claim 6; Page 42; 55pp; French.
 CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O

CC human immune deficiency virus (HIV).
 XX
 SO Sequence 22 AA;
 Query Match 93.7%; Score 119; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 9.6e-09;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LLSWGCGRLVCTYSVQNMET 22
 DB 1 LLSWGCGRLVCTYSVQNMET 22
 RESULT 6
 AAW07346
 ID AAW07346 standard; peptide; 40 AA.
 AC AAW07346;
 XX
 DT 03-JUN-1997 (first entry)
 XX
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).
 XX
 KW Human immunodeficiency virus type 1, HIV-1; env; group M; group O;
 KW C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
 KW primer; hybridization; amplification; PCR; polymerase chain reaction;
 KW immunogen; antibody.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9627013-A1.
 PD 06-SEP-1996.
 XX
 PF 26-FEB-1996; 96WO-FR00294.
 PR 27-FEB-1995; 95FR-0002236.
 XX
 PA (AGSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;
 DR WPI; 1996-412779/41.
 DR N-PSDB; AAT44922.
 XX
 PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 PT immunogens
 XX
 PS Claim 12; Page 34; 71pp; French.
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently
 CC divided into 2 major groups based on the nucleotide sequences of the
 CC env; gp41 gene (env): group M containing sub-groups A-C, and group O
 CC containing the strains AN70 and MWP5180. The invention relates to the
 CC discovery of several new strains of HIV-1 which can be placed in group O,
 CC based on the partial sequences of the C2V3-env, gp41 and gag genes (see
 CC AAT44907-39 and AAW07329-64). The novel strains have been deposited as
 CC retroviruses CNCH I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07
 CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
 CC presented here is from the strain BCF07 (MAN) and corresponds to a
 CC fragment of the gp41 protein encoded by the env gene. The nucleic acids
 CC can be used to detect gp. O HIV-1 strains by hybridisation or (as
 CC primers) by gene amplification, also for screening and typing of such
 CC strains. Peptides encoded by the nucleic acids can be used as immunogens
 CC to raise Ab for detecting gp. O HIV-1.
 XX
 SO Sequence 40 AA;
 Query Match 92.1%; Score 117; DB 17; Length 40;
 Best Local Similarity 86.4%; Pred. No. 3e-08; Indels 0; Gaps 0;
 Matches 19; Conservative 3; Mismatches 0;

QY 1 LLSWGCRGLVCTSVQWNET 22
 DB 19 LLSWGCRGLVCTSVQWNET 40

RESULT 7
 AAW80464 standard; peptide; 22 AA.

AAW80464;
 28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.
 Immune deficiency virus.

WO9845323-A1.
 15-OCT-1998.

06-APR-1998; 98WO-FR00691.
 24-FEB-1998; 98FR-0002212.
 09-APR-1997; 97FR-0004356.

(SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;
 WPI, 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

Claim 6; Page 43; 55pp; French.

AAW80459-74 represent synthetic peptides (either linear or cyclised by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

Sequence 22 AA;

Query Match 91.3%; Score 116; DB 19; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.3e-08;
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCRGLVCTSVQWNET 22
 DB 1 LLSWGCRGLVCTSVQWNET 22

RESULT 8
 AAW80465 standard; peptide; 22 AA.

AAW80465;
 28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.
 Immune deficiency virus.

XX XX WO9845323-A1.
 FN 15-OCT-1998.
 XX
 PD 06-APR-1998; 98WO-FR00691.
 XX
 PF 24-FEB-1998; 98FR-0002212.
 XX
 PR 09-APR-1997; 97FR-0004356.
 XX
 PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 XX
 PI Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;
 XX
 DR WPI; 1998-583190/49.
 XX
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX
 PS Claim 6; Page 43; 55pp; French.

AAW80459-74 represent synthetic peptides (either linear or cyclised by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

Sequence 22 AA;

Query Match 91.3%; Score 116; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2.3e-08;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCRGLVCTSVQWNET 22
 DB 1 LLSWGCRGLVCTSVQWNET 22

RESULT 9
 AAW80463 standard; peptide; 22 AA.

AAW80463;
 28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.
 Immune deficiency virus.

WO9845323-A1.
 15-OCT-1998.

06-APR-1998; 98WO-FR00691.
 24-FEB-1998; 98FR-0002212.
 09-APR-1997; 97FR-0004356.

(SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;
 WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

Claim 6; Page 42; 55pp; French.

XX AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).
XX
SQ Sequence 22 AA;
Query Match 90.6%; Score 115; DB 19; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.1e-08;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LLSWGCRGRLVCTSVQVNET 22
Db 1 LLSWGCRGRLVCTSVQVNET 22
ID AAW80470 standard; peptide; 32 AA.
XX AAW80470;
XX AC
XX 28-JAN-1999 (first entry)
XX DT
XX DE Peptide derived from a conserved sequence of group O human HIV.
XX KM Group O human immune deficiency virus; HIV; detection; infection.
XX OS Synthetic.
XX OS Immune deficiency virus.
XX OS
XX PN WO9845323-A1.
XX PD 15-OCT-1998.
XX PF 06-APR-1998; 98WO-FR00691.
XX PR 24-FEB-1998; 98FR-0002212.
XX PR 09-APR-1997; 97FR-0004356.
XX PA (SNFI) PASTEUR SANOFT DIAGNOSTICS SA.
XX PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;
XX WPI; 1998-583190/49.
PT New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX PS Claim 6; Page 44; 55pp; French.
XX CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).
XX
SQ Sequence 32 AA;
Query Match 89.8%; Score 114; DB 19; Length 32;
Best Local Similarity 86.4%; Pred. No. 6e-08;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LLSWGCRGRLVCTSVQVNET 22
Db 1 LLSWGCRGRLVCTSVQVNET 32
RESULT 11

AAW80459
ID AAW80459 standard; peptide; 22 AA.
XX
XX AAW80459;
AC
XX
XX 28-JAN-1999 (first entry)
XX DT
XX DE Peptide derived from a conserved sequence of group O human HIV.
XX KM Group O human immune deficiency virus; HIV; detection; infection.
XX OS Synthetic.
XX OS Immune deficiency virus.
XX OS
XX PN WO9845323-A1.
XX PD 15-OCT-1998.
XX PF 06-APR-1998; 98WO-FR00691.
XX PR 24-FEB-1998; 98FR-0002212.
XX PR 09-APR-1997; 97FR-0004356.
XX PA (SNFI) PASTEUR SANOFT DIAGNOSTICS SA.
XX PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;
XX WPI; 1998-583190/49.
XX DR
XX PT New synthetic peptide(s) - useful for, e.g. detecting infection by
PT human immune deficiency virus of group O
XX PS Claim 6; Page 42; 55pp; French.
XX CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).
XX
SQ Sequence 22 AA;
Query Match 89.0%; Score 113; DB 19; Length 22;
Best Local Similarity 86.4%; Pred. No. 5.7e-08;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LLSWGCRGRLVCTSVQVNET 22
Db 1 LLSWGCRGRLVCTSVQVNET 22
RESULT 12
AAW80471
ID AAW80471 standard; peptide; 32 AA.
XX
XX AAW80471;
AC
XX
XX 28-JAN-1999 (first entry)
XX DT
XX DE Peptide derived from a conserved sequence of group O human HIV.
XX KM Group O human immune deficiency virus; HIV; detection; infection.
XX OS Synthetic.
XX OS Immune deficiency virus.
XX OS
XX PN WO9845323-A1.
XX PD 15-OCT-1998.
XX PF 06-APR-1998; 98WO-FR00691.
XX

CC	containing the strains AN70 and MP5180. The invention relates to the
CC	discovery of several new strains of HIV-1 which can be placed in group O,
CC	based on the partial sequences of the C2V3-env, gp41 and gag genes (see
CC	AA144907-39 and AA007339-64). The novel strains have been deposited as
CC	retroviruses CNCM 1-1544 (BCF02 (ESS)), 1543 (BCF01 (PAN)), 1546 (BCF07
CC	(MAN)), 1547 (BCF08 (NKO)) and 1545 (BCP03 (POC)). The sequence
CC	presented here is from the strain BCF13 and corresponds to a fragment of
CC	the gp41 protein encoded by the env gene. The nucleic acids can be used
CC	to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene
CC	amplification, also for screening and typing of such strains. Peptides
CC	encoded by the nucleic acids can be used as immunogens to raise Ab for
CC	detecting gp. O HIV-1.
XX	
XX	
SQ	Sequence 40 AA:
Query Match	86.6%; Score 110; DB 17; Length 40;
Best Local Similarity	81.8%; Pred. No. 2,4e-07;
Matches 18; Conservative	3; Mismatches 1; Indels 0; Gaps 0
OY	1 LLSMGCGRLVCYTSTVOMNET 22 : : : 19 LLSMGCKGKRLVCYTSTVEAMNT 40
Dn	
RESULT 14	
ID	AA05565
AC	AA05565 standard; Protein: 113 AA.
XX	
AY05565;	
DT	19-JUL-1999 (first entry)
XX	
DE	HIV-1 group O isolate MP539-PBMC gp41 antigen.
XX	
KW	HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
XX	vaccine; diagnosis; AIDS.
OS	Human immunodeficiency virus type 1.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 65
FT	/note= "encoded by AMW"
FT	Misc-difference 74
FT	/note= "encoded by ATR"
FT	Misc-difference 84
FT	/note= "encoded by GAK"
FT	Misc-difference 86
FT	/note= "encoded by AGY"
PN	WO9904011-A2.
PD	28-JAN-1999.
PE	20-JUL-1998; 98WO-EP04522.
PR	18-JUL-1997; 97EP-0870110.
PA	(INNO-) INNOGENETICS NV.
P1	Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
DR	MP1; 1999-132255/11.
DR	N-PSDB; AA05565.
PT	New isolated HIV-1 group O strains - used to produce
PT	polynucleotides, antigens and antibodies for use in diagnosis and in
PT	vaccines for prevention of HIV-1 infection
PS	Claim 3; Fig 6; 16zpp; English.
XX	
XX	The present sequence is an antigen of the gp41 protein of HIV-1
XX	group O (Outlier) strain MP539-PBMC, a Cameroon isolate. The
XX	invention relates to new HIV-1 group O antigens (see AA05546-625),
CC	

```

CC antigen and detecting the antigen-antibody complex. The monoclonal
CC antibodies of the invention would be used to ensure that the reagents
CC provided to detect HIV-1 group O antibody were performing properly. The
CC monoclonal antibodies may also can be immobilised on a matrix and used
CC for affinity purification of specific HIV-1 group O-derived proteins
CC from cell cultures or biological tissues. The monoclonal antibodies can
CC also be used for generating chimeric antibodies for therapeutic use.
CC Different synthetic, recombinant or purified antibodies which identify
CC different epitopes of HIV antigens can be used in combination in assay to
CC diagnose, evaluate, or prognosticate HIV disease condition. The
CC monoclonal antibodies are also useful for differentiating HIV-1 Group O
CC antigens from HIV-group M and HIV-2 antigens. Sequences AAY77369-Y77375
CC represent recombinant HIV-1 group O env antigens encoded by the synthetic
CC genes AA290280-290286. The recombinant HIV-1 env proteins contain
CC various deletions relative to the native HAM12 isolate env protein
CC (AAY77376). The recombinant HIV-1 group O antigens were purified and used
CC to screen hybridoma cultures.
CC
XX
SQ Sequence 200 AA;
CC
Query Match 86.6%; Score 110; DB 21; Length 200;
Best Local Similarity 77.3%; Pred. No. 1e-06;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0.
QY 1 LLSWGCGRRLVCTSYQNMET 22
DB 112 LNLWGCKGRILCYTSVKMNET 133

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:36 ; Search time 9.95238 Seconds
(without alignments)
65.040 Million cell updates/sec

Title: US-09-147-362a-8

Sequence: 1 LLSWGCRGLVCTSVQNMET 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	92.1	40	3	US-08-894-699-39
2	117	92.1	40	4	US-09-444-410-39
3	110	86.6	40	3	US-08-894-699-68
4	110	86.6	40	4	US-09-444-410-68
5	110	86.6	215	2	US-08-912-129A-58
6	110	86.6	245	2	US-08-912-129A-58
7	110	86.6	373	2	US-08-912-129A-52
8	110	86.6	460	2	US-08-912-129A-60
9	110	86.6	490	2	US-08-912-129A-50
10	110	86.6	618	2	US-08-912-129A-54
11	110	86.6	873	4	US-08-912-129A-61
12	109	85.8	37	4	US-08-817-441-94
13	109	85.8	104	4	US-08-817-441-100
14	108	85.0	33	4	US-09-433-428D-6
15	107	84.3	33	4	US-09-433-428D-25
16	107	84.3	40	3	US-08-894-699-36
17	107	84.3	40	4	US-09-444-410-36
18	107	84.3	356	1	US-08-602-713-12
19	107	84.3	356	1	US-08-989-493-12
20	106	83.5	37	4	US-08-817-441-86
21	106	83.5	41	3	US-08-894-699-69
22	106	83.5	41	4	US-09-444-410-69
23	106	83.5	200	4	US-08-965-056-104
24	105	82.7	23	4	US-08-817-441-30
25	105	82.7	41	3	US-09-433-428D-30
26	105	82.7	41	3	US-08-894-699-67
27	105	82.7	41	4	US-09-444-410-67

28	104	81.9	33	4	US-09-433-428D-8	Sequence 8, Appli
29	104	81.9	40	3	US-08-894-699-41	Sequence 41, Appl
30	104	81.9	40	3	US-08-894-699-42	Sequence 42, Appl
31	104	81.9	40	4	US-09-444-410-41	Sequence 41, Appl
32	104	81.9	40	4	US-09-444-410-42	Sequence 42, Appl
33	103	81.1	40	3	US-08-894-699-37	Sequence 37, Appl
34	103	81.1	40	4	US-09-444-410-37	Sequence 37, Appl
35	102	80.3	40	3	US-08-894-699-40	Sequence 40, Appl
36	102	80.3	40	4	US-09-444-410-40	Sequence 40, Appl
37	101	79.5	23	4	US-09-433-428D-68	Sequence 68, Appl
38	101	79.5	33	4	US-09-433-428D-1	Sequence 1, Appli
39	101	79.5	33	4	US-09-433-428D-4	Sequence 4, Appli
40	101	79.5	33	4	US-09-433-428D-7	Sequence 7, Appli
41	101	79.5	33	4	US-09-433-428D-15	Sequence 15, Appl
42	101	79.5	42	3	US-08-894-699-66	Sequence 66, Appl
43	101	79.5	42	4	US-09-444-410-66	Sequence 66, Appl
44	100	78.7	33	4	US-09-433-428D-5	Sequence 5, Appli
45	100	78.7	33	4	US-09-433-428D-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-08-894-699-39
Sequence 39, Application US/08894699

Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SENTOB

APPLICANT: LOUSSEST-AJAKA, IBITISSAM

APPLICANT: LY, THOI-NUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

NUMBER OF INVENTIONS: VIRUSES, AND USES THEREOF

CORRESPONDENCE ADDRESS: 81

ADDRESS: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESS: P. C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,699

FILING DATE: 01-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294

FILING DATE: 26-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-894-699-39

Query Match 92.1%; Score 117; DB 3; Length 40;
Best Local Similarity 86.4%; Pred. No. 1.7e-10;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 L1SSWCGRGLVCTYSVQWNET 22
||:||||:||||:||||:||||:
DB 19 L1NSWCGKRGRLVCTYSVKWNET 40

RESULT 2

US-09-444-410-39
Sequence 39, Application US/09444410
Patent No. 6270975

GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEST-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-39

Query Match 92.1%; Score 117; DB 4; Length 40;
Best Local Similarity 86.4%; Pred. No. 1.7e-10;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 L1SSWCGRGLVCTYSVQWNET 22
||:||||:||||:||||:||||:
DB 19 L1NSWCGKRGRLVCTYSVKWNET 40

RESULT 3
US-08-894-699-68
Sequence 68, Application US/08894699
Patent No. 6030769

GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEST-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-68

Query Match 86.6%; Score 110; DB 3; Length 40;
Best Local Similarity 81.8%; Pred. No. 1.7e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 L1SSWCGRGLVCTYSVQWNET 22
||:||||:||||:||||:||||:
DB 19 L1NSWCGKRGRLVCTYSVKWNET 40

RESULT 4

US-09-444-410-68
Sequence 68, Application US/09444410
Patent No. 6270975

GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEST-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-68

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MALER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-68
Query Match 86.6%; Score 110; DB 4; Length 40;
Best Local Similarity 81.8%; Pred. No. 1.7e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
1 LLSWGCGRLVCTYSVNMNT 22
||:||||:||||:||||:
19 LLSWGCGRLVCTYSVNMNT 40
RESULT 5
US-08-912-129A-58
Sequence 58, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITEK, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
City: Abbott Park
STATE: IL
COUNTRY: USA

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckerts, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-912-129A-58
Query Match 86.6%; Score 110; DB 2; Length 215;
Best Local Similarity 77.3%; Pred. No. 9.9e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
1 LLSWGCGRLVCTYSVNMNT 22
||:||||:||||:||||:
127 LLSWGCGRLVCTYSVNMNT 148
RESULT 6
US-08-912-129A-48
Sequence 48, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITEK, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
City: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

```

: NAME: Danckerts, Andreas M.
: REGISTRATION NUMBER: 32,652
: REFERENCE/DOCKET NUMBER: 6109.US.01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 847-937-9803
: TELEFAX: 847-938-2623
:
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 245 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-912-129A-48
:
Query Match 86.6%; Score 110; DB 2; Length 245;
Best Local Similarity 77.3%; Pred. No. 1,1e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
:
: 1 LLSWGCRGLVCTYSVQNMET 22
: |||:||||:||||:||||
:
Db 127 LNLWGCKRGLICTYSVQNMET 148
:
RESULT 7
US-08-912-129A-52
: Sequence 52, Application US/08912129A
: Patent No. 5922533
: GENERAL INFORMATION:
: APPLICANT: VALLARI, ANADRUZELA S.
: APPLICANT: HACKETT, JOHN JR.
: APPLICANT: HICKMAN, ROBERT K.
: APPLICANT: VARITER, VINCENT A. JR.
: APPLICANT: NECKLAWS, ELIZABETH A.
: APPLICANT: GOLDEN, ALAN M.
: APPLICANT: BRENNAN, CATHERINE A.
: APPLICANT: DEVARE, SUSHIL G.
: TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
: NUMBER OF SEQUENCES: 89
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Abbott Laboratories
: STREET: 100 Abbott Park Road
: CITY: Abbott Park
: STATE: IL
: COUNTRY: USA
: ZIP: 60064-3500
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: MS-DOS (Windows 95)
: SOFTWARE: Microsoft Word (ASCII format output)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/912,129A
: FILING DATE: 15-AUG-1997
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Danckerts, Andreas M.
: REGISTRATION NUMBER: 32,652
: REFERENCE/DOCKET NUMBER: 6109.US.01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 847-937-9803
: TELEFAX: 847-938-2623
:
: TEXT:
: INFORMATION FOR SEQ ID NO: 52:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 373 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear

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      : MOLECULE TYPE: protein
US-08-912-129A-52

Query Match          86.6%; Score 110; DB 2; Length 373;
Best Local Similarity 77.3%; Pred. No. 1,7e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 LLSWGCGRGLVCTSYVMNET 22
   |||::|||::|||::|||
Db       127 LLNLWGCGRLLICTYSVKMET 148

RESULT 8
US-08-912-129A-60
; Sequence 60, Application US/08912129A
; Patent No. 5925533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANADRUZELA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARITEK, VINCENT A. JR.
; APPLICANT: NECKLAW, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEVARE, SUSHLI G.
; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,129A
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckerts, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 460 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-912-129A-60

Query Match          86.6%; Score 110; DB 2; Length 460;
Best Local Similarity 77.3%; Pred. No. 2,2e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 LLSWGCGRGLVCTSYVMNET 22
   |||::|||::|||::|||
Db       372 LLNLWGCGRLLICTYSVKMET 393

RESULT 9

```

US-08-912-129A-50
; Sequence 50, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANANDRUZELA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARITER, VINCENT A. JR.
; APPLICANT: NECKLAWS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEVARE, SUSHIL G.
; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,129A
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckerts, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 490 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 8-912-129A-50

Query Match 86.6%; Score 110; DB 2; Length 490;
Best Local Similarity 77.3%; Pred No. 2.3e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCTSVQNNET 22
DB 372 LNLWGCKRGLICTSVKNNET 393

RESULT 10
US-08-912-129A-54
; Sequence 54, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANANDRUZELA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARITER, VINCENT A. JR.
; APPLICANT: NECKLAWS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEVARE, SUSHIL G.
; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION

NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,129A
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckerts, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-129A-54

Query Match 86.6%; Score 110; DB 2; Length 618;
Best Local Similarity 77.3%; Pred. No. 2.3e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCTSVQNNET 22
DB 372 LNLWGCKRGLICTSVKNNET 393

RESULT 11
US-08-912-129A-61
; Sequence 61, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANANDRUZELA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARITER, VINCENT A. JR.
; APPLICANT: NECKLAWS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEVARE, SUSHIL G.
; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ. ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-912-129A-61

Query Match 86.6%; Score 110; DB 2; Length 873;
Best Local Similarity 77.3%; Pred. No. 4.2e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCRGLVCTSYVNNET 22
Db 601 LNLWGCKRGLICTSYVNNET 622

RESULT 12
US-08-817-441-94
Sequence 94, Application US/08817441
Patent No. 6399294
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
APPLICANT: CLAVEL, FRANCOISE
APPLICANT: BORMAN, ANDREW
APPLICANT: OUILLENT, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: MONTAGNIER, LUC
APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE
APPLICANT: COHEN, JAOUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,441
FILING DATE: 11-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9502526

FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ. ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-441-94

Query Match 85.8%; Score 109; DB 4; Length 37;
Best Local Similarity 77.3%; Pred. No. 2.2e-09;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCRGLVCTSYVNNET 22
Db 14 LNLWGCKRGLICTSYVNNET 35

RESULT 13
US-08-817-441-100
Sequence 100, Application US/08817441
Patent No. 6399294
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
APPLICANT: CLAVEL, FRANCOISE
APPLICANT: BORMAN, ANDREW
APPLICANT: OUILLENT, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: MONTAGNIER, LUC
APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE
APPLICANT: COHEN, JAOUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,441
FILING DATE: 11-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000

Search completed: May 29, 2003, 10:41:28
Job time : 9.95238 secs

TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-817-441-100

Query Match 85.8%; Score 109; DB 4; Length 104;
Best Local Similarity 77.3%; Pred. No. 6.5e-09;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCRGLVCTYSVQWNET 22
||:||||:||||:||||:
Db 45 LLSWGCRGLVCTYSVQWNET 66

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; Sequence 6, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leye, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-6

Query Match 85.0%; Score 108; DB 4; Length 33;
Best Local Similarity 85.0%; Pred. No. 2.8e-09;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCRGLVCTYSVQWNET 20
||:||||:||||:||||:
Db 14 LLSWGCRGLVCTYSVQWNET 33

|||||
; Sequence 25, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leye, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 25
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-25

Query Match 84.3%; Score 107; DB 4; Length 33;
Best Local Similarity 85.0%; Pred. No. 3.9e-09;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCRGLVCTYSVQWNET 20
||:||||:||||:||||:
Db 14 LLSWGCRGLVCTYSVQWNET 33

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:39:21 ; Search time 19.0317 Seconds
(without alignments)
117.011 Million cell updates/sec

Title: US-09-147-362a-8

Perfect score: 127

Sequence: 1 LLSWGCRGRILVCTYSVQNMET 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	86.6	215	1	US-08-911-824-58 Sequence 58, Appl
2	110	86.6	245	1	US-08-911-824-48 Sequence 48, Appl
3	110	86.6	281	1	US-08-911-824-120 Sequence 120, Appl
4	110	86.6	373	1	US-08-911-824-52 Sequence 52, Appl
5	110	86.6	460	1	US-08-911-824-60 Sequence 60, Appl
6	110	86.6	488	1	US-08-911-824-95 Sequence 95, Appl
7	110	86.6	490	1	US-08-911-824-50 Sequence 50, Appl
8	110	86.6	526	1	US-08-911-824-97 Sequence 97, Appl
9	110	86.6	618	1	US-08-911-824-54 Sequence 54, Appl
10	110	86.6	706	1	US-08-911-824-93 Sequence 93, Appl
11	110	86.6	735	1	US-08-911-824-91 Sequence 91, Appl
12	110	86.6	873	1	US-08-911-824-61 Sequence 61, Appl
13	109	85.8	37	9	US-10-026-741-94 Sequence 94, Appl
14	109	85.8	104	9	US-10-026-741-100 Sequence 100, Appl
15	106	83.5	37	9	US-10-026-741-86 Sequence 86, Appl
16	106	83.5	200	10	US-09-854-816-104 Sequence 104, Appl
17	105	82.7	23	9	US-10-026-741-30 Sequence 30, Appl
18	100	78.7	35	9	US-10-026-741-101 Sequence 101, Appl
19	100	78.7	37	9	US-10-026-741-7 Sequence 7, Appl

ALIGNMENTS

20	100	78.7	37	9	US-10-026-741-90	Sequence 90, Appl
21	100	78.7	351	9	US-10-026-741-47	Sequence 47, Appl
22	100	78.7	877	9	US-10-026-741-102	Sequence 102, Appl
23	99	78.0	24	9	US-10-026-741-34	Sequence 34, Appl
24	98	77.2	37	9	US-10-026-741-88	Sequence 88, Appl
25	96	75.6	213	10	US-09-854-816-103	Sequence 103, Appl
26	93	73.2	23	9	US-09-388-847-4	Sequence 4, Appl
27	93	73.2	23	12	US-10-000-321-2	Sequence 2, Appl
28	93	73.2	35	9	US-09-886-156-62	Sequence 62, Appl
29	93	73.2	35	9	US-09-886-150-62	Sequence 62, Appl
30	93	73.2	35	9	US-09-886-149-62	Sequence 62, Appl
31	93	73.2	35	9	US-09-886-159-62	Sequence 62, Appl
32	93	73.2	146	12	US-10-000-321-10	Sequence 10, Appl
33	93	73.2	204	10	US-09-854-816-105	Sequence 105, Appl
34	93	73.2	351	9	US-09-886-156-46	Sequence 46, Appl
35	93	73.2	351	9	US-09-886-150-46	Sequence 46, Appl
36	93	73.2	351	9	US-09-886-149-46	Sequence 46, Appl
37	93	73.2	351	9	US-09-886-159-46	Sequence 46, Appl
38	85	66.9	268	10	US-09-854-816-39	Sequence 39, Appl
39	83	65.4	37	9	US-10-026-741-84	Sequence 84, Appl
40	83	65.4	204	10	US-09-854-816-106	Sequence 106, Appl
41	83	65.4	1231	9	US-10-059-271-94	Sequence 8, Appl
42	82	64.6	22	9	US-10-059-271-8	Sequence 81, Appl
43	81	63.8	198	10	US-09-854-816-81	Sequence 82, Appl
44	80	63.0	37	9	US-10-026-741-82	Sequence 77, Appl
45	80	63.0	198	10	US-09-854-816-77	

```

RESULT 1
US-08-911-824-58
; Sequence 58, Application US/08911824
; Publication No. US20030004323A1
GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824.
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-8PL
US-08-911-824-58

Query Match      86.6%; Score 110; DB 1; Length 215;
Best Local Similarity 77.3%; Pred. No. 2.9e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db      127 LLSWGCRGRILVCTYSVQNMET 148

RESULT 2
US-08-911-824-48
; Sequence 48, Application US/08911824
; Publication No. US20030004323A1
GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories

```

```

; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-9PL
08-911-824-48
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```

Query Match      86.6%; Score 110; DB 1; Length 245;
Best Local Similarity 77.3%; Pred. No. 3.2e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1  LLSWGCGRGLVCTYSVQNMET 22
DB      127  LNLWGCKGRLLICTYSVKMNET 148
```

RESULT 3

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US-08-911-824-120
; Sequence 120, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-15PL
US-08-911-824-120
```

```

Query Match      86.6%; Score 110; DB 1; Length 281;
Best Local Similarity 77.3%; Pred. No. 3.7e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1  LLSWGCGRGLVCTYSVQNMET 22
DB      127  LNLWGCKGRLLICTYSVKMNET 148
```

RESULT 4

```

US-08-911-824-52
; Sequence 52, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
```

```

; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-11PL
US-08-911-824-52
```

```

Query Match      86.6%; Score 110; DB 1; Length 373;
Best Local Similarity 77.3%; Pred. No. 4.8e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1  LLSWGCGRGLVCTYSVQNMET 22
DB      127  LNLWGCKGRLLICTYSVKMNET 148
```

RESULT 5

```

US-08-911-824-60
; Sequence 60, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pGO-8CKS
US-08-911-824-60
```

```

Query Match      86.6%; Score 110; DB 1; Length 460;
Best Local Similarity 77.3%; Pred. No. 5.9e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1  LLSWGCGRGLVCTYSVQNMET 22
DB      372  LNLWGCKGRLLICTYSVKMNET 393
```

RESULT 6

```

US-08-911-824-95
; Sequence 95, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
```


APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 95
LENGTH: 488
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-14PL
US-08-911-824-95

Query Match 86.6%; Score 110; DB 1; Length 488;
Best Local Similarity 77.3%; Pred. No. 6.2e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCTSVQNMET 22
DB 127 LNLWGCGRGLICTSVKMNET 148

RESULT 7
US-08-911-824-50
Sequence 50, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 490
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-9CKS
US-08-911-824-50

Query Match 86.6%; Score 110; DB 1; Length 490;
Best Local Similarity 77.3%; Pred. No. 6.2e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCTSVQNMET 22
DB 372 LNLWGCGRGLICTSVKMNET 393

RESULT 8
US-08-911-824-97
Sequence 97, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.

APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 97
LENGTH: 526
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-15CKS
US-08-911-824-97

Query Match 86.6%; Score 110; DB 1; Length 526;
Best Local Similarity 77.3%; Pred. No. 6.6e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCTSVQNMET 22
DB 372 LNLWGCGRGLICTSVKMNET 393

RESULT 9
US-08-911-824-54
Sequence 54, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 618
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-11CKS
US-08-911-824-54

Query Match 86.6%; Score 110; DB 1; Length 618;
Best Local Similarity 77.3%; Pred. No. 7.7e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCTSVQNMET 22
DB 372 LNLWGCGRGLICTSVKMNET 393

RESULT 10
US-08-911-824-93
Sequence 93, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.

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/ APPLICANT: Hickman, Robert K.
/ APPLICANT: Devare, Sushil G.
/ TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
/ TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
/ FILE REFERENCE: 6165.US.O1
/ CURRENT APPLICATION NUMBER: US/08/911,824
/ CURRENT FILING DATE: 1997-08-15
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 93
/ LENGTH: 706
/ TYPE: PRT
/ ORGANISM: Human Immunodeficiency Virus
/ FEATURE:
/ OTHER INFORMATION: Encodes recombinant protein pCO-13CKS
US-08-911-824-93

Query Match      86.6%; Score 110; DB 1; Length 706;
Best Local Similarity 77.3%; Pred. No. 8.7e-06;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 LLSWGCRGLVCTSVQNMET 22
        ||:||||:||||:||||:
Db      618 LNLWGCKGRILCTSVKMMET 639

RESULT 11
US-08-911-824-91
/ Sequence 91, Application US/08911824
/ Publication No. US2003000433A1
/ GENERAL INFORMATION:
/ APPLICANT: Abbott Laboratories
/ APPLICANT: Hackett, John R., Jr.
/ APPLICANT: Yamaguchi, Julie
/ APPLICANT: Golden, Alan M.
/ APPLICANT: Brennan, Catherine A.
/ APPLICANT: Hickman, Robert K.
/ APPLICANT: Devare, Sushil G.
/ TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
/ TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
/ FILE REFERENCE: 6165.US.O1
/ CURRENT APPLICATION NUMBER: US/08/911,824
/ CURRENT FILING DATE: 1997-08-15
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 91
/ LENGTH: 736
/ TYPE: PRT
/ ORGANISM: Human Immunodeficiency Virus
/ FEATURE:
/ OTHER INFORMATION: Encodes recombinant protein pCO-12CKS
US-08-911-824-91

Query Match      86.6%; Score 110; DB 1; Length 736;
Best Local Similarity 77.3%; Pred. No. 9.1e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 LLSWGCRGLVCTSVQNMET 22
        ||:||||:||||:||||:
Db      618 LNLWGCKGRILCTSVKMMET 639

RESULT 12
US-08-911-824-61
/ Sequence 61, Application US/08911824
/ Publication No. US2003000432A1
/ GENERAL INFORMATION:
/ APPLICANT: Abbott Laboratories
/ APPLICANT: Hackett, John R., Jr.
/ APPLICANT: Yamaguchi, Julie
/ APPLICANT: Golden, Alan M.
/ APPLICANT: Brennan, Catherine A.
/ APPLICANT: Hickman, Robert K.
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/ APPLICANT: Devare, Sushil G.
/ TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
/ TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
/ FILE REFERENCE: 6165 US.O1
/ CURRENT APPLICATION NUMBER: US/08/911,824
/ CURRENT FILING DATE: 1997-08-15
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 61
/ LENGTH: 873
/ TYPE: PRT
/ ORGANISM: Human Immunodeficiency Virus
/ FEATURE:
/ OTHER INFORMATION: HIV-1 Group O Isolate HAM112
US-08-911-824-61

Query Match      86.6%; Score 110; DB 1; Length 873;
Best Local Similarity 77.3%; Pred. No. 1.1e-07;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 LLSWGCRGLVCTSVQNMET 22
        ||:||||:||||:||||:
Db      601 LNLWGCKGRILCTSVKMMET 622

RESULT 13
US-10-026-741-94
/ Sequence 94, Application US/10026741
/ Publication No. US2003004960A1
/ GENERAL INFORMATION:
/ APPLICANT: CHARNEAU, PIERRE
/ APPLICANT: CLAVEL, FRANCOISE
/ APPLICANT: BORMAN, ANDREW
/ APPLICANT: QUILLENT, CAROLINE
/ APPLICANT: GUERARD, DENISE
/ APPLICANT: MONTAGNIER, LUC
/ APPLICANT: COHEN, JACQUES
/ APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
/ SUBTYPE) ANTIGENS
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ STREET: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/026,741
/ FILING DATE: 27-Dec-2001
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 08/817,441
/ FILING DATE: 31-AUG-1998
/ APPLICATION NUMBER: PCT/FR 95/01391
/ FILING DATE: 20-OCT-1995
/ APPLICATION NUMBER: FR 9412554
/ FILING DATE: 20-OCT-1994
/ APPLICATION NUMBER: FR 9502526
/ FILING DATE: 03-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meyers, Kenneth J.
/ REGISTRATION NUMBER: 25,146
/ REFERENCE/DOCKET NUMBER: 03260.6005-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
```

INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-10-026-741-94

Query Match 85.8%; Score 109; DB 9; Length 37;
Best Local Similarity 77.3%; Pred. No. 7.7e-09;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCYTSVQNNET 22
||:||||:|||||||
DB 14 LLMWGCRGKALCYTSVQNNET 35

US-10-026-741-100
Sequence 100, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
OUILLENT, CAROLINE
GUETARD, DENISE
MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQUELINE
COHEN, JACQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fimegan, Henderson, Farabow, Garrett &
Dunnet, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-026-741-100

Query Match 85.8%; Score 109; DB 9; Length 104;
Best Local Similarity 77.3%; Pred. No. 2e-08;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCYTSVQNNET 22
||:||||:|||||||
DB 45 LLMWGCRGKALCYTSVQNNET 66

RESULT 15
US-10-026-741-86
Sequence 86, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
OUILLENT, CAROLINE
GUETARD, DENISE
MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQUELINE
COHEN, JACQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fimegan, Henderson, Farabow, Garrett &
Dunnet, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-026-741-86

Query Match 83.5%; Score 106; DB 9; Length 37;
Best Local Similarity 77.3%; Pred. No. 2.1e-08;

Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLSWGCRRLVCTSYQNNET 22
||| |||:|||||:|
Db 14 LLSWGCRRLVCTSYQNNRT 35

Search completed: May 29, 2003, 11:03:57
Job time : 19.0317 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:06 ; Search time 10.8254 Seconds
(without alignments)
195.370 Million cell updates/sec

Title: US-09-147-362A-8

Perfect score: 127

Sequence: 1 LLSWGCRGRIVCYTSVQNMNET 22

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues
1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	85.8	104	2	GP41 ENV protein -
2	106	83.5	863	2	env polypeptide pr
3	100	78.7	877	2	env polypeptide pr
4	83	65.4	854	1	env polypeptide pr
5	82	64.6	357	2	env polypeptide pr
6	82	64.6	358	2	env polypeptide pr
7	81	63.8	358	2	env polypeptide pr
8	81	63.8	358	2	env polypeptide pr
9	80	63.0	443	2	env polypeptide pr
10	80	63.0	853	2	env polypeptide pr
11	80	63.0	855	1	env polypeptide pr
12	79	62.2	357	2	env polypeptide pr
13	79	62.2	357	2	env polypeptide pr
14	79	62.2	357	2	env polypeptide pr
15	79	62.2	357	2	env polypeptide pr
16	79	62.2	357	2	env polypeptide pr
17	79	62.2	358	2	env polypeptide pr
18	79	62.2	445	2	env polypeptide pr
19	79	62.2	445	2	env polypeptide pr
20	79	62.2	843	1	env polypeptide pr
21	79	62.2	847	2	env polypeptide pr
22	79	62.2	847	2	env polypeptide pr
23	79	62.2	852	1	env polypeptide pr
24	79	62.2	852	1	env polypeptide pr
25	79	62.2	854	2	env polypeptide pr
26	79	62.2	855	2	env polypeptide pr
27	79	62.2	856	1	env polypeptide pr
28	79	62.2	856	1	env polypeptide pr
29	79	62.2	856	1	env polypeptide pr

30	79	62.2	859	1	VCLJMN	env polypeptide pr
31	79	62.2	861	1	VCLJLV	env polypeptide pr
32	79	62.2	861	1	VCLJSC	env polypeptide pr
33	79	62.2	868	1	VCLJH4	env polypeptide pr
34	78.5	61.8	855	2	A457J3	env transmembrane
35	78	61.4	786	2	S28084	env polypeptide pr
36	77	60.6	856	1	A44963	env polypeptide pr
37	76	59.8	846	1	VCLJND	env polypeptide pr
38	74.5	58.7	859	1	VCLJST	env polypeptide pr
39	74.5	58.7	859	2	S24571	env polypeptide pr
40	74.5	58.7	885	2	S04322	env polypeptide pr
41	74.5	58.7	886	2	T11555	env polypeptide pr
42	73	57.5	729	1	VCLJXK	env polypeptide pr
43	73	57.5	861	1	VCLJKB	env polypeptide pr
44	72.5	57.1	151	2	S30448	env polypeptide pr
45	72.5	57.1	151	2	S30453	env polypeptide pr

ALIGNMENTS

RESULT 1

GP41 ENV protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999

C:Accession: S52930
R: Cohen, J.H.M.; Guetard, D.; Philibert, F.; Chameret, S.; Tabary, T.; Montagnier, L.; de
submitted to the EMBL Data Library, January 1995

A:Description: A novel HIV-1 O strain illustrates the diversity of the O group.

A:Reference number: S52929

A:Accession: S52930

A:Status: Preliminary

A:Molecule type: genomic RNA

A:Residues: 1-104 <COH>

A:Cross-references: EMBL:X84328; NID:G695526; PIDN:CA59066.1; PID:G695527

C:Superfamily: type B retrovirus env polypeptide

Query Match 85.8%; Score 109; DB 2; Length 104;

Best Local Similarity 77.3%; Pred. No. 1.1e-08;

Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCRGRIVCYTSVQNMNET 22
DB 45 LLSWGCRGRIVCYTSVQNMNET 66

RESULT 2

gp41 polypeptide - human immunodeficiency virus type 1 (strain Ant70)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999

C:Accession: A53034
R: Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborcht, B.; van der Groen,

J. Virol. 68, 1586-1596, 1994

A:Title: Genomic cloning and complete sequence analysis of a highly divergent African hu

A:Reference number: A53034; MUID:94149849; PMID:8107220

A:Accession: A53034

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-863 <VAN>

A:Cross-references: GB:L02587

C:Superfamily: type B retrovirus env polypeptide

C:Keywords: polypeptide

Query Match 83.5%; Score 106; DB 2; Length 863;

Best Local Similarity 77.3%; Pred. No. 1.9e-07;

Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCRGRIVCYTSVQNMNET 22
DB 594 LLSWGCRGRIVCYTSVQNMNET 615

RESULT 3

S49197
envelope protein precursor - human immunodeficiency virus type 1 (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
C/Accession: S49197
R/Steuiler, H.; Borman, A.M.; Quillent, C.; Guetard, D.; Chameret, S.; Cohen, J.; Remy, submitted to the EMBL Data Library, July 1994
A/Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi
A/Reference number: S49197
A/Accession: S49197
A/Molecule type: DNA
A/Residues: 1-877 <CHA>
A/Cross-references: EMBL:X80020; NID:G510516; PIDN:CAA56323.1; PID:G510517
A/Experimental source: Isolate VAV
C/Superfamily: type E retrovirus env polypotein
C/Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein
F.1-30/DNA: signal sequence #status predicted <Sig>
F.1-535/Product: coat protein gp120 #status predicted <CP1>
F.56-877/Product: coat protein gp41 #status predicted <CP2>
F.598-716/DNA: transmembrane #status predicted <TMN>
F.59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,

Query Match 78.7%; Score 100; DB 2; Length 877;
Best Local Similarity 68.2%; Pred. No. 1.4e-06;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCRGLVCTYSVQNNET 22
DB 607 LLLMGCKRNLICYSVKNNKT 628

RESULT 4

VCLJ51
env polypotein precursor - simian immunodeficiency virus SIVCPZ
N/Alternate names: coat polypotein
N/Contents: coat protein gp120; coat protein gp41
C/Species: simian immunodeficiency virus SIVCPZ
A/Note: host Pan troglodytes (chimpanzee)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
A/Accession: S09990
R/Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A/Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A/Reference number: S09993; MUID:90259077; PMID:2188136
A/Accession: S09990
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-854 <HUE>
A/Cross-references: EMBL:X52154; NID:G58866; PIDN:CAA36407.1; PID:G58874

C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polypotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F.1-30/DNA: signal sequence #status predicted <Sig>
F.31-500/Product: coat protein gp120 #status predicted <CP1>
F.501-854/Product: coat protein gp41 #status predicted <CP2>
F.501-517/DNA: transmembrane #status predicted <TM1>
F.675-693/DNA: transmembrane #status predicted <TM2>
F.805-822/DNA: transmembrane #status predicted <TM3>
F.113,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 65.4%; Score 83; DB 1; Length 854;
Best Local Similarity 54.5%; Pred. No. 0.00038;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLSWGCRGLVCTYSVQNNET 22
DB 582 ILGLMGCSGKAVCYTTPMNN 603

RESULT 5

S21990

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 20
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21990; S70423
R/Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ
A/Reference number: S21990
A/Accession: S21990
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176
R/Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70423
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-332, 'X', 334-357 <STE2>
A/Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176
C/Superfamily: type E retrovirus env polypotein

Query Match 64.6%; Score 82; DB 2; Length 357;
Best Local Similarity 65.0%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCRGLVCTYSVQNN 20
DB 93 LLGIMGCSGRLICTTAVPWN 112

RESULT 6

S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:G60186; PIDN:CAA43616.1; PID:G60187
R/Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STE2>
A/Cross-references: EMBL:X61352; NID:G60186
C/Superfamily: type E retrovirus env polypotein

Query Match 64.6%; Score 82; DB 2; Length 358;
Best Local Similarity 65.0%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCRGLVCTYSVQNN 20
DB 94 LLGIMGCSGRLICTTAVPWN 113

RESULT 7

S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C/Accession: S22000
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A/Reference number: S21990
A/Accession: S22000
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STB>
A/Cross-references: EMBL:X61351
C/Superfamily: type E retrovirus env polyprotein

Query Match 63.8%; Score 81; DB 2; Length 358;
Best Local Similarity 65.0%; Pred. No. 0.00035;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCGRGLVCTTVPMN 113
94 LLSWGCGRGLVCTTVPMN 113

RESULT 8
S70417
env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: patient 3B
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C/Accession: S70417
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70417
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STB>
A/Cross-references: EMBL:X61351; NID:G60184; PIDN:CAA43614.1; PID:G60185
C/Superfamily: type E retrovirus env polyprotein

Query Match 63.8%; Score 81; DB 2; Length 358;
Best Local Similarity 65.0%; Pred. No. 0.00035;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCGRGLVCTTVPMN 20
94 LLSWGCGRGLVCTTVPMN 113

ULT 9
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N/Alternate names: coat polyprotein
N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C/Accession: C41621
R/Burger, H.; Weiser, B.; Flaherty, K.; Guila, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 11236-11240, 1991
A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A/Reference number: A41621; MUID:92107924; PMID:1763038
A/Accession: C41621
A/Molecule type: DNA
A/Residues: 1-443 <STB>
A/Cross-references: GB:M77230; NID:G328631; PIDN:AA03792.1; PID:G555015
A/Note: This virus was isolated from the mother's sexual partner
C/Genetics:
A/Status: preliminary
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polyp
F1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F1-252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F1-252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F1-24-443/Domain: transmembrane #status predicted <TM>
F1-23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 63.0%; Score 80; DB 2; Length 443;
Best Local Similarity 54.5%; Pred. No. 0.00058;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCGRGLVCTTVPMN 22
332 LLSWGCGRGLVCTTVPMN 353

RESULT 10
S54384
env polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C/Accession: S54384
R/Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A/Reference number: S54377
A/Accession: S54384
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-853 <THE>
A/Cross-references: EMBL:M2639; NID:G329377; PIDN:AAA45370.1; PID:G329385
C/Keywords: polyprotein

Query Match 63.0%; Score 80; DB 2; Length 853;
Best Local Similarity 54.5%; Pred. No. 0.001;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCGRGLVCTTVPMN 22
589 LLSWGCGRGLVCTTVPMN 610

RESULT 11
VCL42R
env polyprotein precursor - human immunodeficiency virus Zr-6
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus Zr-6
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C/Accession: D26192
R/Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A/Title: Molecular characterization of human immunodeficiency virus from Zaïre: nucleot
A/Reference number: A26192; MUID:87248097; PMID:3036660
A/Accession: D26192
A/Molecule type: DNA
A/Residues: 1-855 <STB>
A/Cross-references: GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45380.1; PID:G329403
C/Genetics:
A/Status: preliminary
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F1-19/Domain: signal sequence #status predicted <SIG>
F1-20-855/Product: env polyprotein #status predicted <MAT>
F1-20-500/Product: exterior membrane glycoprotein #status predicted <TM>
F1-501-855/Product: transmembrane glycoprotein #status predicted <TM>
F1-87,129,140,145,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 63.0%; Score 80; DB 1; Length 855;
Best Local Similarity 54.5%; Pred. No. 0.001;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCGRGLVCTTVPMN 22
591 LLSWGCGRGLVCTTVPMN 612

RESULT 12

S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70420; S22006
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
A:Experimental source: patient L
A>Note: Submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 62.2%; Score 79; DB 2; Length 357;
Best Local Similarity 60.0%; Pred. No. 0.00067;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 LSSWGCRGLVCTSVQWN 20
DB 93 LIGWGCGSKLICITTVPMN 112

RESULT 13
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21994
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STB1>
A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STB2>
A:Cross-references: EMBL:X61355; NID:g60179
C:Superfamily: type E retrovirus env polyprotein

Query Match 62.2%; Score 79; DB 2; Length 357;
Best Local Similarity 60.0%; Pred. No. 0.00067;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 LSSWGCRGLVCTSVQWN 20
DB 93 LIGWGCGSKLICITTVPMN 112

RESULT 14
S22004
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 4B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S22004; S70419
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990

A:Accession: S22004
A:Molecule type: DNA
A:Residues: 1-357 <STB1>
A:Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292, 'X', 294-357 <STB2>
A:Cross-references: EMBL:X61353; NID:g60188
C:Superfamily: type E retrovirus env polyprotein

Query Match 62.2%; Score 79; DB 2; Length 357;
Best Local Similarity 60.0%; Pred. No. 0.00067;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 LSSWGCRGLVCTSVQWN 20
DB 93 LIGWGCGSKLICITTVPMN 112

RESULT 15
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129
A:Experimental source: patient 27L
A>Note: Submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 62.2%; Score 79; DB 2; Length 357;
Best Local Similarity 60.0%; Pred. No. 0.00067;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 LSSWGCRGLVCTSVQWN 20
DB 93 LIGWGCGSKLICITTVPMN 112

Search completed: May 29, 2003, 10:40:24
Job time: 10.8254 sec


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FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 854 AA; 95803 MW; 2E249AFAD4F2D9B3 CRC64;

Query Match 65.4%; Score 83; DB 1; Length 854;
Best Local Similarity 54.5%; Pred. No. 3.3e-05;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 1 LSSWCGRGLVCTSYVQNET 22
582 ILGLWGCGSKAVCTTVPNNNS 603

RESULT 2
ENV_HV122 STANDARD; PRT; 853 AA.
ID ENV_HV122
AC P12487;
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
OC Viruses; Retrovirda; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
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DR EMBL; M22639; AAA45370.1; -
DR HIV; M22639; ENV52226.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00515; GP120.1.
DR Pfam; PF00517; GP41.1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 2 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 3 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 415 BY SIMILARITY.
FT CARBOHYD 87 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B08CBAFF7008 CRC64;

Query Match 63.0%; Score 80; DB 1; Length 853;
Best Local Similarity 54.5%; Pred. No. 9.6e-05;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 1 LSSWCGRGLVCTSYVQNET 22
589 ILGLWGCGSKAVCTTVPNNNS 610

RESULT 3
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126
AC P04580;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retrovirda; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
RA Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
RA Schoeneman G., Curran J., Kalyanaraman V.S., Lutch P.A.,
RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from
RT zaire; nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene.";
RL Gene 52:71-82(1987).
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DR EMBL; K03458; AAA45380.1; -
DR PIR; D26192; VCUJZR.

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Thu May 29 15:25:57 2003

DR HIV; K03458; ENV526.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 510
 FT CHAIN 511 855
 FT DISULFID 53 73
 FT DISULFID 118 207
 FT DISULFID 125 198
 FT DISULFID 130 155
 FT DISULFID 220 249
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 FT CARBOHYD 87 129
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 FT CARBOHYD 673 673
 SQ SEQUENCE 855 AA; 96971 MW; 384D3D6E239C3457 CRC64;
 Query Match 63.0%; Score 80; DB 1; Length 855;
 Best Local Similarity 54.5%; Pred. No. 9,6e-05;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 LLSMCGRGLVCTVQNNET 22
 Db 591 LLSMCGRGLVCTVQNNET 612
 ID ENV_HV12 STANDARD; PRT; 843 AA.
 AC P35961;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor (Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN ENV.
 OS Human immunodeficiency virus type 1 (TU-2 isolate) (HIV-1).

OC Viruses; Retrovirus; Retroviridae; Lentivirus.
 ON NCBI_TaxID=36377;
 RX MEDLINE=93021387; PubMed=1404605;
 RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
 Shaw G.M.;
 RT "Complete nucleotide sequence, genome organization, and biological
 properties of human immunodeficiency virus type 1 in vivo: evidence
 for limited defectiveness and complementation.";
 CC J. Virol. 66:6587-6600(1992).
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 CC -----
 CC EMBL; M33258; -; NOT_ANNOTATED_CDS.
 CC PIR; H44001; H44001.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 489
 FT CHAIN 490 843
 FT TRANSMEM 738 755
 FT DISULFID 53 73
 FT DISULFID 118 201
 FT DISULFID 125 192
 FT DISULFID 130 155
 FT DISULFID 214 243
 FT DISULFID 224 235
 FT DISULFID 292 326
 FT DISULFID 373 432
 FT DISULFID 380 405
 FT CARBOHYD 87 87
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 Query Match 62.2%; Score 79; DB 1; Length 843;
 Best Local Similarity 60.0%; Pred. No. 0.00014;


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FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96466 MW; CD1E33D73A5BCAE CRC64;

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Query Match 62.2%; Score 79; DB 1; Length 847;
Best Local Similarity 60.0%; Pred. No. 0.90014;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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QY 1 LLSMCGRGLVCTSVQVN 20
Db 583 LIGWCGSKLICTTAVPMN 602

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RESULT 7
ENV_HV1B8 STANDARD; PRT; 851 AA.
AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.

```

```

Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11684;

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OX NCB1_TaxID=11684;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111133; PubMed=2578615;
RA Ratner L., Haseilane W., Patarca R., Liyak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafaleki J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Laubenberger J.A., Papas T.S., Chirayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal P.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).

```

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CC or send an email to license@isb-sib.ch).

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CC EMBL: K02011; AAA4661.1; -
CC DR HIV; K02011; ENV5B88.
CC DR GlycosultedB; P04582; -

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DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 506
FT CHAIN 507 851
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 166
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 440
FT DISULFID 385 413
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 401 401
FT CARBOHYD 443 443
FT CARBOHYD 458 458
FT CARBOHYD 606 606
FT CARBOHYD 611 611
FT CARBOHYD 620 620
FT CARBOHYD 632 632
FT CARBOHYD 669 669
FT CARBOHYD 745 745
FT CARBOHYD 811 811
SQ SEQUENCE 851 AA; 96644 MW; D16A3C908577B5F1 CRC64;

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Query Match 62.2%; Score 79; DB 1; Length 851;
Best Local Similarity 60.0%; Pred. No. 0.00014;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 LLSMCGRGLVCTSVQVN 20
Db 587 LIGWCGSKLICTTAVPMN 606

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RESULT 8
ENV_HV1B8 STANDARD; PRT; 852 AA.
AC P12488;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
OX Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCB1_TaxID=11693;
RN [1]
RP SEQUENCE FROM N.A.

```

Query Match	Similarity	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232
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Oy	1	L1SSWCGRGLVACTSYQVM	20
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Dd	588	L1G1WGCSGKLTCTTANPMN	607
 RESULT 9			
ID	ENV_HV1S3	STANDARD;	PRT; 852 AA.
AC	P19549;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Envelope polypeptide GP160 precursor [containing: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
GN	ENV.		
OS	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).		
OC	Retroviridae; Retrovirus.		
OX	NCBI_Taxid=11690;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90317906; Pubmed=2370688;		
RA	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;		
RT	"Human immunodeficiency virus type 1 cellular host range,		
RT	replication, and cytopathicity are linked to the envelope region of		
RL	the viral genome.";		
RL	J. Virol. 64:4016-4020(1990).		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; M38427; AAA45067.1; .		
DR	HIV; M38427; ENVSEF33.		
DR	InterPro; IPR000328; Env GP41.		
DR	InterPro; IPR000777; GP120.		
DR	Pfam; PF00516; GP120; 1.		
DR	Pfam; PF00517; GP41; 1.		
Kw	AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane;		
Kw	Signal.		
FT	SIGNAL	31	BY SIMILARITY.
FT	CHAIN	1	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	BY SIMILARITY.
FT	DISULFID	118	BY SIMILARITY.
FT	DISULFID	125	BY SIMILARITY.
FT	DISULFID	130	BY SIMILARITY.
FT	DISULFID	219	BY SIMILARITY.
FT	DISULFID	229	BY SIMILARITY.
FT	DISULFID	297	BY SIMILARITY.
FT	DISULFID	377	BY SIMILARITY.
FT	DISULFID	384	BY SIMILARITY.
FT	CARBOHYD	87	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	129	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	136	N-LINKED (GLCNAC. .) (POTENTIAL).
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FT	CARBOHYD	142	N-LINKED (GLCNAC. .) (POTENTIAL).
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FT	CARBOHYD	159	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	189	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	198	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	242	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	263	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	277	N-LINKED (GLCNAC. .) (POTENTIAL).
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FT	CARBOHYD	296	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	332	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	339	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	355	N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 852 AA: 96663 MW: 27878230910D CRC64;
 Query Match 62.2%; Score 79; DB 1; Length 852;
 Best Local Similarity 60.0%; Pred. No. 0.00014;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 LLSWGCGRGLVCTYSVQWN 20
 588 LIGWCGSGRLCTTTPWN 607
 RESULT 10
 ID ENV_HV1MP STANDARD; PRT; 853 AA.
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentiviruses.
 NC NCBI_TaxID=11704;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90317877; PubMed=1695254;
 RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C., Wasik A.;
 RT "Cloning and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis.";
 RL J. Virol. 64:3792-3803 (1990).
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 DR EMBL; M33943; AAA44850.1; -
 DR HIV; M33943; ENVSMFA.
 DR InterPro; IPR000328; ENV GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KM SIGNAL.
 FT CHAIN 1 30
 FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFID 510 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 203 BY SIMILARITY.
 FT DISULFID 126 194 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 157 245 BY SIMILARITY.
 FT DISULFID 226 327 BY SIMILARITY.
 FT DISULFID 239 443 BY SIMILARITY.
 FT DISULFID 376 443 BY SIMILARITY.

FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA: 96912 MW: 337789386F22ABA CRC64;
 Query Match 62.2%; Score 79; DB 1; Length 853;
 Best Local Similarity 60.0%; Pred. No. 0.00014;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 LLSWGCGRGLVCTYSVQWN 20
 DB 590 LIGWCGSGRLCTTTPWN 609
 RESULT 11
 ID ENV_HV1A2 STANDARD; PRT; 855 AA.
 AC P03378;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentiviruses.
 NC NCBI_TaxID=11685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85090453; PubMed=2578227;
 RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S., Stempien M.M., Brown-Shiner S.L., Gee W.W., Renard A., Randolph A., Levy J.A., Dina D., Luciw P.A.;
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)." Science 227:484-492 (1985).
 RL Science 227:484-492 (1985).
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 DR EMBL; K02007; AAB59882.1; -

DR PIR: A03976; VCUA2.
 DR HIV; KO2007; ENV5SF2.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL. 1 29
 FT CHAIN 30 509
 FT CHAIN 510 855
 FT DISULFID 53 73
 FT DISULFID 118 208
 FT DISULFID 125 199
 FT DISULFID 130 155
 FT DISULFID 221 250
 FT DISULFID 231 242
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 FT CARBOHYD 190 190
 FT CARBOHYD 200 200
 FT CARBOHYD 233 233
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 SQ SEQUENCE 855 AA; 97438 MW; A3BC0573AAC41A2 CRC64;
 Query Match 62.2%; Score 79; DB 1; Length 855;
 Best Local Similarity 60.0%; Pred. No. 0.00014;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 LLSWGRRLVCTSYQNM 20
 Db 591 LLSWGRRLVCTSYQNM 610
 RESULT 12
 ENV_HVIOY STANDARD; PRT; 855 AA.
 AC P20886;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120), Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148544; PubMed=2559749;
 RA Huec T., Daza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.,
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
 RT individual presenting an atypical western blot".
 RL AIDS 3:707-715(1989).
 CC MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
 CC HEALTHY GABONESE INDIVIDUAL.
 CC -----
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 CC or send an email to license@isb.ch).
 CC -----
 CC EMBL: M26727; AAA83397.1; -
 CC HIV; M26727; ENV5OY1.
 CC InterPro: IPR000328; Env GP41.
 CC InterPro: IPR000777; GP120.
 CC Pfam: PF00516; GP120; 1.
 CC Pfam: PF00517; GP41; 1.
 CC AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL. 1 29
 FT CHAIN 30 509
 FT CHAIN 510 855
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
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 FT CARBOHYD 142 142
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 FT CARBOHYD 815 815
 SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADDE2DA CRC64;
 Query Match 62.2%; Score 79; DB 1; Length 855;
 Best Local Similarity 60.0%; Pred. No. 0.00014;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

ID	ENV_HV1B1	STANDARD	PRT	856 AA
AC	P03375			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OC	Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).			
OS	Vitruves; Retrovird viruses; Retroviridae; Lentiviridae.			
OX	NCBI_TaxID=11678;			
RN	[1]			
	SEQUENCE FROM N.A.			
	MEDLINE=8511123; PubMed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,			
RA	Joseph S.F., Doran E.R., Rafaleki J.A., Whitehorn E.A.,			
RA	Baumeister K., Ivanoff L., Peteway S.R.Jr., Pearson M.L.,			
RA	Lautebecker J.F., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,			
RT	Wong-Staal F.;			
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RL	Nature 313:277-284(1985).			
RN	[2]			
RT	DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.			
RP	MEDLINE=90285159; PubMed=235006;			
RX	Leonard C.K., Speilman M.W., Riddle L., Harris R.J., Thomas J.N.,			
RA	Gregory T.J.;			
RT	"Assignment of intrachain disulfide bonds and characterization of			
RT	potential glycosylation sites of the type 1 recombinant human			
RT	immunodeficiency virus envelope glycoprotein (gp120) expressed in			
RL	Chinese hamster ovary cells";			
RL	J. Biol. Chem. 265:10373-10382(1990).			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M15654; AAA44205.1; -.			
DR	PIR; A03973; VCLJH3			
DR	HIV; M15654; ENVSH102.			
DR	InterPro; IPR000328; ENV_GP41.			
DR	Pfam; PF00516; GP120. 1.			
DR	Pfam; PF00517; GP41. 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	511	
FT	CHAIN	512	856	
FT	DISULFID	54	74	
FT	DISULFID	119	205	
FT	DISULFID	126	196	
FT	DISULFID	131	157	
FT	DISULFID	218	247	
FT	DISULFID	228	239	
FT	DISULFID	296	331	
FT	DISULFID	378	445	
FT	DISULFID	385	418	
FT	CARBOHYD	88	88	
FT	CARBOHYD	136	136	
FT	CARBOHYD	141	141	
FT	CARBOHYD	156	156	
FT	CARBOHYD	160	160	
FT	CARBOHYD	160	160	

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CC FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
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CC FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .)
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CC FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)
CC FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .)
CC SQ SEQUENCE 856 AA; 97224 MW; 0BFEB1A8931B827 CRC64;

Query Match 62.2%; Score 79; DB 1; Length 856;
Best Local Similarity 60.0%; Pred. No. 0.00014;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLSWGCGRILVCYTSVOMN 20
Db 592 LLGIWGCGSKRLCTTAVPMN 611

RESULT 14
ENV_HVII2 STANDARD; PRT; 856 AA.
ID ENV_HVII2
AC P04578; O09779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAY-2000 (Rel. 39, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate).
OC Viruses; Retroid viruses; Retroviridae; Lentivirae.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A. MEDLINE=87299196; PubMed=3040055;
RX Rattner L., Fisher A., Jagodzinski L.L., Mitsuya H., Lion R.-S., RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS RT virus";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Rattner L., Fisher A., Jagodzinski L.L., Mitsuya H., Lion R.-S., RA Gallo R.C., Wong-Staal F.;
RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
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DR EMBL, K03455; AAB50262.1; -.

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DR EMBL: AF039399; AAB99976.1; -
DR EMBL: AF033819; AAC82596.1; -
DR HIV: K03455; ENVSHXB2.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
signal.
KM SIGNAL.
FT CHAIN 1 30
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SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107E0 CRC64;

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Best Local Similarity 60.04; Pred. No. 0.00014;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLSWGRRLVYTSYQVN 20
Db 592 LLSWGRRLVYTSYQVN 611

RESULT 15
ENV_HVILM STANDARD; PRT; 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
CJ ENV.

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OS Human immunodeficiency virus type 1 (TM12.3 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
CC -----
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CC -----
DR EMBL: U12055; AAA7690.1; -
DR GlycoSuiteDB: Q70626; -
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
signal.
FT SIGNAL.
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FT CHAIN 511 511
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FT CARBOHYD 624 624
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FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF76687 CRC64;

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Query Match 62.2%; Score 79; DB 1; Length 856;
 Best Local Similarity 60.0%; Pred. No. 0.00014;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 LLSWGCRGRVLCYTSVQWN 20
 |||||:|:|:|:
 Db 592 LIGWGCSGKLCCTTAAPWN 611

Search completed: May 29, 2003, 10:36:59
 Job time : 5.4127 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:32:35 ; Search time 22.6984 Seconds
(without alignments)
199.707 Million cell updates/sec

Title: US-09-147-362A-8

Sequence: 1 LLSWGCGRRLVCYTSVQNNET 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

al number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	92.1	216	15	Q91EC5 human immun
2	114	89.8	135	15	Q9DOL9 human immun
3	114	89.0	209	15	Q91E66 human immun
4	112	88.2	219	15	Q91E86 human immun
5	110	86.6	116	15	Q40458 human immun
6	110	86.6	124	15	Q91HU7 human immun
7	110	86.6	126	15	Q91HV1 human immun
8	110	86.6	130	15	Q91HU9 human immun
9	110	86.6	218	15	Q91E95 human immun
10	110	86.6	230	15	Q91E82 human immun
11	110	86.6	240	15	Q91E32 human immun
12	110	86.6	536	15	Q91E85 human immun
13	110	86.6	538	15	Q91E85 human immun
14	110	86.6	872	15	Q8Q7H0 human immun
15	110	86.6	879	15	Q9W1U9 human immun
16	110	86.6	880	15	Q8Q7H1 human immun

17	110	86.6	882	15	Q8Q7R9 human immun
18	110	86.6	887	15	Q8Q7H6 human immun
19	110	86.6	887	15	Q8Q7G9 human immun
20	110	86.6	900	15	Q9QNZ8 human immun
21	109	85.8	104	15	Q76163 human immun
22	109	85.8	216	15	Q91E87 human immun
23	109	85.8	535	15	Q91E82 human immun
24	108	85.0	125	15	Q91HU8 human immun
25	108	85.0	230	15	Q91EA9 human immun
26	108	85.0	238	15	Q91E81 human immun
27	108	85.0	242	15	Q91E81 human immun
28	108	85.0	529	15	Q91E82 human immun
29	107	84.3	114	15	Q40448 human immun
30	107	84.3	116	15	Q40459 human immun
31	107	84.3	137	15	Q91HV5 human immun
32	107	84.3	172	15	Q91EB3 human immun
33	107	84.3	177	15	Q91EB0 human immun
34	107	84.3	208	15	Q91EA3 human immun
35	107	84.3	219	15	Q91EC8 human immun
36	107	84.3	227	15	Q91E99 human immun
37	107	84.3	234	15	Q91EC2 human immun
38	107	84.3	342	15	O11942 human immun
39	107	84.3	418	15	Q36547 human immun
40	107	84.3	502	15	Q91EB3 human immun
41	107	84.3	871	15	Q57074 human immun
42	107	84.3	871	15	Q8Q712 human immun
43	107	84.3	876	15	Q8Q7H3 human immun
44	106	83.5	114	15	Q40456 human immun
45	106	83.5	114	15	O40472 human immun

ALIGNMENTS

RESULT 1				
ID	Q91EC5	PRELIMINARY;	PRT;	216 AA.
AC	Q91EC5;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	GP41 (Fragment).			
ENV.				
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_Taxid=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BCF07;			
RA	Roques P., Robertson D., Sandrine S., Christel D., Francois S., Philippe M.;			
RT	"Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."			
RL	Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AJ236394; CAB96243.1; -			
DR	InterPro: IPR000328; Env_Gp41.			
DR	Pfam: PF00517; GP41; 1.			
KW	Transmembrane.			
FT	NON TER 1			
FT	TER 216			
SO	SEQUENCE 216 AA; 25027 MW; 413AB9BB1B4FC9A CRC64;			
Query Match				
Best Local Similarity 92.1%; Score 117; DB 15; Length 216;				
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
QY	1	LLSWGCRRLVCYTSVQNNET 22		
		: : :		
DB	47	LLSWGCRRLVCYTSVQNNET 68		
RESULT 2				
Q9DOL9	PRELIMINARY;	PRT;	135 AA.	
ID	Q9DOL9			

AC Q9D0L9;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SP-M1321;
 RX MEDLINE=20584646; PubMed=1153079;
 RA Ortiz M., Munoz U., Bernal A., Rodriguez A., Zorruguino A.,
 RA Vaillo J., Salas A., Moreno A., Garcia-Salz A.;
 RT "Molecular Characterization of Non-B HIV Type 1 Subtypes from Africa
 in Spain";
 RL AIDS Res. Hum. Retroviruses 16:1967-1971 (2000).
 DR EMBL; AF255939; AAG36894.1; -;
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KM Transmembrane.
 FT NON_TER 1
 FT NON_TER 135
 SQ SEQUENCE 135 AA; 16285 MW; D34B9F77318B36 CRC64;

Query Match 89.8%; Score 114; DB 15; Length 135;
 Best Local Similarity 81.8%; Pred. No. 3e-10;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCRGLVCTSVQNNET 22
 Db 48 LLSWGCRGLVCTSVQNNST 69

RESULT 3
 Q9IE66 PRELIMINARY; PRT; 209 AA.
 ID Q9IE66;
 AC Q9IE66;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Env polypeptide, gp41 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCF107;
 RA Roques P., Robertson D., Diamond F., Souquiere S., Mauciere P.,
 RA Delienne C., Brun-Vezinet F., Dormont D., Simon F.O.;
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ238862; CAB96300.1; -;
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KM Transmembrane.
 FT NON_TER 1
 FT NON_TER 209
 SQ SEQUENCE 209 AA; 24116 MW; 91AC9BE2BF74883 CRC64;

Query Match 89.0%; Score 113; DB 15; Length 209;
 Best Local Similarity 81.8%; Pred. No. 6.7e-10;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCRGLVCTSVQNNET 22
 Db 56 LLSWGCRGLVCTSVQNNET 77

RESULT 4
 Q9IEB6

ID Q9IEB6 PRELIMINARY; PRT; 219 AA.
 AC Q9IEB6;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Gp41 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCF14;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ236404; CAB96252.1; -;
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KM Transmembrane.
 FT NON_TER 1
 FT NON_TER 219
 SQ SEQUENCE 219 AA; 25353 MW; F65829B801520D91 CRC64;

Query Match 88.2%; Score 112; DB 15; Length 219;
 Best Local Similarity 81.8%; Pred. No. 1e-09;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCRGLVCTSVQNNET 22
 Db 57 LLSWGCRGLVCTSVQNNNT 78

RESULT 5
 Q40458 PRELIMINARY; PRT; 116 AA.
 ID Q40458;
 AC Q40458;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Envelope transmembrane glycoprotein (Fragment).
 GN Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GROUP O;
 RA Bihollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;
 RT "Molecular characterization of envelope transmembrane glycoprotein of
 RT 14 new human immunodeficiency virus type 1 group O strains from
 RT different African countries";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y09774; CAA70913.1; -;
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KM Transmembrane.
 FT NON_TER 1
 FT NON_TER 116
 SQ SEQUENCE 116 AA; 13865 MW; 540F5B3B7AD849D8 CRC64;

Query Match 86.6%; Score 110; DB 15; Length 116;
 Best Local Similarity 77.3%; Pred. No. 1.1e-09;
 Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCRGLVCTSVQNNET 22
 Db 39 LLSWGCRGLVCTSVQNNKT 60

RESULT 6
 Q9IHU7 PRELIMINARY; PRT; 124 AA.
 ID Q9IHU7

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AC Q91HU7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CM768;
RA MEDLINE=20386754; PubMed=10933623;
RX Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229237; AAF71914.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT SEQUENCE 124 AA; 15187 MW; 105D515F114450F8 CRC64;
SQ
Query Match 86.6%; Score 110; DB 15; Length 124;
Best Local Similarity 77.3%; Pred. No. 1.2e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L1SSWGCGRGLVCTSVQNMET 22
Db 33 L1NLWGCKGRGLVCTSVKMNKT 54

RESULT 7
O91HV1 PRELIMINARY; PRT; 126 AA.
ID Q91HV1;
AC Q91HV1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97S203;
RA MEDLINE=20386754; PubMed=10933623;
RX Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229233; AAF71910.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT SEQUENCE 126 AA; 15169 MW; 13FB101ECDCFODDD CRC64;
SQ
Query Match 86.6%; Score 110; DB 15; Length 126;
Best Local Similarity 81.8%; Pred. No. 1.2e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L1SSWGCGRGLVCTSVQNMET 22
Db 40 L1NLWGCKGRGLVCTSVKMNKT 61
```

```
RESULT 8
O91HU9 PRELIMINARY; PRT; 130 AA.
ID Q91HU9;
AC Q91HU9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CM798;
RA MEDLINE=20386754; PubMed=10933623;
RX Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229235; AAF71912.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT SEQUENCE 130 AA; 15593 MW; 5385789A336344EA CRC64;
SQ
Query Match 86.6%; Score 110; DB 15; Length 130;
Best Local Similarity 77.3%; Pred. No. 1.2e-09;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 L1SSWGCGRGLVCTSVQNMET 22
Db 40 L1NLWGCKGRGLVCTSVKMNKT 61

RESULT 9
O91E95 PRELIMINARY; PRT; 218 AA.
ID Q91E95;
AC Q91E95;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF51.
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ236425; CAB96273.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT SEQUENCE 218 AA; 25243 MW; E7F0E1E20EF79FA8 CRC64;
SQ
Query Match 86.6%; Score 110; DB 15; Length 218;
Best Local Similarity 77.3%; Pred. No. 2.1e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L1SSWGCGRGLVCTSVQNMET 22
Db 54 L1SSWGCCKGRGLVCTSVKMNKT 75
```

RESULT 10

Q9IEB2 PRELIMINARY; PRT; 230 AA.
AC Q9IEB2; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
EMBL: AJ236408; CAB96256.1; -
InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT TER 230
SQ SEQUENCE 230 AA; 26705 MW; C1F744F82F51302D CRC64;

Query Match 86.6%; Score 110; DB 15; Length 230;
Best Local Similarity 77.3%; Pred. No. 2.2e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSMGCGRGLVCTSYVNMET 22
DB 55 LLLMGCKGRLLCTYSVKMNET 76

RESULT 11

Q9IEB2 PRELIMINARY; PRT; 240 AA.
AC Q9IEB2; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TM, GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF11;
RA Roques P., Robertson D., Sousquiere S., Darnold F., Mauciere P.,
Deplienne C., Brun-Vezinet F., Dormont D., Simon F.O.;
RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."
Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
EMBL: AJ243365; CAB96335.1; -
InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT TER 240
SQ SEQUENCE 240 AA; 27723 MW; 1E206E8D491A197 CRC64;

Query Match 86.6%; Score 110; DB 15; Length 240;
Best Local Similarity 77.3%; Pred. No. 2.3e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSMGCGRGLVCTSYVNMET 22
DB 60 LLLMGCKGRLLCTYSVKMNET 81

RESULT 12

Q9IEB5 PRELIMINARY; PRT; 536 AA.
AC Q9IEB5; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Roques P., Robertson D., Darnold F., Sousquiere S., Mauciere P.,
Deplienne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."
Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
EMBL: AJ133062; CAB96223.1; -
InterPro: IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
FT TER 536
SQ SEQUENCE 536 AA; 60419 MW; 0F533ABA08FE552 CRC64;

Query Match 86.6%; Score 110; DB 15; Length 536;
Best Local Similarity 77.3%; Pred. No. 5.1e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSMGCGRGLVCTSYVNMET 22
DB 361 LLLMGCKGRLLCTYSVKMNET 382

RESULT 13

Q9IED5 PRELIMINARY; PRT; 538 AA.
AC Q9IED5; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Roques P., Robertson D., Darnold F., Sousquiere S., Mauciere P.,
Deplienne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."
Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
EMBL: AJ133072; CAB96233.1; -
InterPro: IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
FT TER 538
SQ SEQUENCE 538 AA; 60777 MW; B3C9E6A233FEF1D CRC64;

Query Match 86.6%; Score 110; DB 15; Length 538;
Best Local Similarity 77.3%; Pred. No. 5.1e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSMGCGRGLVCTSYVNMET 22
DB 60 LLLMGCKGRLLCTYSVKMNET 81

Db 374 LLSWGCKGKLCYTSVKMNTT 395

RESULT 14

0807H0 PRELIMINARY; PRT; 872 AA.

AC 0807H0. PRELIMINARY; PRT; 872 AA.

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE Envelope glycoprotein.

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RN [1]

RX MEDLINE=98CMA453;

RX MEDLINE=21849375; PubMed=11860674;

Ymaguchi J., Vallart A.S., Swanson P., Bodelle P., Kapue L., Ngansop C., Zekeng L., Gurler L.G., Devare S.G., Brennan C.A.; "Evaluation of HIV Type 1 Group O Isolates: Identification of Five Phylogenetic Clusters."

RT AIDS Res. Hum. Retroviruses 18:269-282(2002).

RL EMBL, AF383251; AAL98873.1; .

SQ SEQUENCE 872 AA; 98344 MW; 91D37F60053827E3 CRC64;

Query Match 86.6%; Score 110; DB 15; Length 872;

Best Local Similarity 77.3%; Pred. No. 8.3e-09;

Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCYTSVQWNET 22

Db 602 LLSWGCKGKLCYTSVKMNTT 623

RESULT 15

Q9WIU9 PRELIMINARY; PRT; 879 AA.

AC Q9WIU9;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE GP160 precursor.

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

[1]

SEQUENCE FROM N.A.

RC STRAIN=VI686;

RX MEDLINE=99223950; PubMed=10207543;

RA Janssens W., Heyndrickx L., Van der Auwera G., Nkengasong J., Beirnaert E., Vereecken K., Coppens S., Willems B., Franssen K., Peeters M., Ndunde P., Delaporte E., Van der Groen G.; "Interpatient genetic variability of HIV-1 Group O.";

RL AIDS 13:41-48(1999).

[2]

SEQUENCE FROM N.A.

RP STRAIN=VI686;

RX MEDLINE=96426454; PubMed=8828748;

RA Delaporte E., Janssens W., Peeters M., Buve A., Dibaba G., Perret J.L., Ditsambou V., Georges Courbot M.C., Georges A., Bourgeois A., Samb B., Henzel D., Heyndrickx L., Franssen K., Van der Groen G., Larouz B., Mbe J.R.; "Epidemiological and Molecular characteristics of HIV infection in Gabon (1986 - 1994).";

RT AIDS 10:903-910(1996).

RL EMBL, X96526; CAA65373.1; .

DR InterPro: IPR000328; Env GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS: Coat protein; Glycoprotein; Polyprotein; Signal; Transmembrane.

FT SIGNAL 1 29

FT CHAIN 30 524 POTENTIAL.

FT CHAIN 132 156 GP120.

FT CHAIN 164 200 V1.

FT CHAIN 302 335 V2.

FT CHAIN 395 427 V3.

FT CHAIN 458 475 V4.

FT CHAIN 475 475 V5.

FT CHAIN 525 879 GP41.

SQ SEQUENCE 879 AA; 99099 MW; BC6422ADDPLA3409 CRC64;

Query Match 86.6%; Score 110; DB 15; Length 879;

Best Local Similarity 77.3%; Pred. No. 8.3e-09;

Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRLVCYTSVQWNET 22

Db 605 LLSWGCKGKLCYTSVKMNTT 626

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Job time : 22.6984 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20 ; Search time 21.3333 Seconds

(without alignments)
99.938 Million cell updates/sec

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Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	16	AAW80467	Peptide derived fr
2	91	100.0	22	AAW80461	Peptide derived fr
3	91	100.0	22	AAW80462	Peptide derived fr
4	88	96.7	16	AAW80468	Peptide derived fr
5	88	96.7	22	AAW80472	Peptide derived fr
6	88	96.7	22	AAW80465	Peptide derived fr
7	88	96.7	28	AAW80473	Peptide derived fr
8	88	96.7	33	AAW80473	Peptide derived fr
9	88	96.7	33	AAW80473	Peptide derived fr
10	88	96.7	40	AAW80473	Peptide derived fr

11	88	96.7	40	AAW80467	Peptide derived fr
12	87	95.6	22	AAW80463	Peptide derived fr
13	86	94.5	33	AAW80463	Peptide derived fr
14	86	94.5	40	AAW80463	Peptide derived fr
15	85	93.4	33	AAW80469	Peptide derived fr
16	85	93.4	33	AAW80469	Peptide derived fr
17	85	93.4	33	AAW80469	Peptide derived fr
18	84	92.3	40	AAW80474	Peptide derived fr
19	82	90.1	22	AAW80460	Peptide derived fr
20	82	90.1	23	AAW80460	Peptide derived fr
21	82	90.1	23	AAW80460	Peptide derived fr
22	82	90.1	24	AAW80460	Peptide derived fr
23	82	90.1	24	AAW80460	Peptide derived fr
24	82	90.1	32	AAW80460	Peptide derived fr
25	82	90.1	33	AAW80460	Peptide derived fr
26	82	90.1	33	AAW80460	Peptide derived fr
27	82	90.1	33	AAW80460	Peptide derived fr
28	82	90.1	33	AAW80460	Peptide derived fr
29	82	90.1	33	AAW80460	Peptide derived fr
30	82	90.1	41	AAW80460	Peptide derived fr
31	82	90.1	42	AAW80460	Peptide derived fr
32	82	90.1	116	AAW80460	Peptide derived fr
33	82	90.1	117	AAW80460	Peptide derived fr
34	82	90.1	129	AAW80460	Peptide derived fr
35	82	90.1	129	AAW80460	Peptide derived fr
36	82	90.1	173	AAW80460	Peptide derived fr
37	82	90.1	200	AAW80460	Peptide derived fr
38	82	90.1	200	AAW80460	Peptide derived fr
39	82	90.1	715	AAW80460	Peptide derived fr
40	81	89.0	23	AAW80460	Peptide derived fr
41	81	89.0	23	AAW80460	Peptide derived fr
42	81	89.0	23	AAW80460	Peptide derived fr
43	81	89.0	23	AAW80460	Peptide derived fr
44	81	89.0	23	AAW80460	Peptide derived fr
45	81	89.0	23	AAW80460	Peptide derived fr

ALIGNMENTS

RESULT 1	AAW80467	standard; peptide: 16 AA.
ID	AAW80467	
AC	AAW80467	
XX		
DT	28-JAN-1999	(first entry)
XX		
DE	Peptide derived from a conserved sequence of group O human HIV.	
XX		
KW	Group O human immune deficiency virus; HIV; detection; infection.	
XX		
OS	Synthetic.	
XX		
FN	Immune deficiency virus.	
PD	WO9845323-A1.	
XX		
PD	15-OCT-1998.	
XX		
PF	06-APR-1998; 98NO-FR00691.	
XX		
FR	24-FEB-1998; 98FR-0002212.	
PR	09-APR-1997; 97FR-0004356.	
XX		
PA	(SNFI) PASTEUR SANOFI DIAGNOSTICS SA.	
XX		
PI	Cheneaux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;	
XX		
DR	WPI; 1998-583190/49.	
XX		
PT	New synthetic peptide(s) - useful for, e.g. detecting infection by	
XX	human immune deficiency virus of group O	

PS Claim 6; Page 43; 55pp; French.
 XX
 CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 19; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCYTS 16
 |||||
 Db 1 LLSWGCKGRIVCYTS 16

BLT 2

AAW80461
 ID AAW80461 standard; peptide; 22 AA.

AC AAW80461;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.

OS Immune deficiency virus.

PN MO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 91; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCYTS 16
 |||||
 Db 1 LLSWGCKGRIVCYTS 16

RESULT 3
 AAW80462
 ID AAW80462 standard; peptide; 22 AA.

AC AAW80462;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

PN MO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 91; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCYTS 16
 |||||
 Db 1 LLSWGCKGRIVCYTS 16

RESULT 4

AAW80468
 ID AAW80468 standard; peptide; 16 AA.

AC AAW80468;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

PN MO9845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

```

XX 24-FEB-1998; 98FR-0002212.
PR 09-APR-1997; 97FR-0004356.
XX
XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.
XX Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;
XX WPI; 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 43; 55pp; French.
XX
XX AAW80459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O
XX human immune deficiency virus (HIV).
XX
SQ Sequence 16 AA;

Query Match 96.7%; Score 88; DB 19; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTS 16
   ||:|||||
Db 1 LLSWGCKGRIVCYTS 16

RESULT 5
AAW80472
ID AAW80472 standard; peptide; 22 AA.
XX
XX AAW80472;
XX
XX 28-JAN-1999 (first entry)
XX
XX Peptide derived from a conserved sequence of group O human HIV.
XX
XX Group O human immune deficiency virus; HIV; detection; infection.
XX
XX Synthetic.
XX
XX Immune deficiency virus.
XX
XX WO9845323-A1.
XX
XX 15-OCT-1998.
XX
XX 06-APR-1998; 98WO-FR00691.
XX
XX 24-FEB-1998; 98FR-0002212.
XX
XX 09-APR-1997; 97FR-0004356.
XX
XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.
XX
XX Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;
XX
XX WPI; 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 44; 55pp; French.
XX
XX AAW80459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O
XX

```

```

CC human immune deficiency virus (HIV).
XX
XX Sequence 22 AA;
SQ
XX
XX Query Match 96.7%; Score 88; DB 19; Length 22;
XX Best Local Similarity 93.8%; Pred. No. 3.7e-06;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTS 16
   ||:|||||
Db 6 LLSWGCKGRIVCYTS 21

RESULT 6
AAW80466
ID AAW80466 standard; peptide; 22 AA.
XX
XX AAW80466;
XX
XX 28-JAN-1999 (first entry)
XX
XX Peptide derived from a conserved sequence of group O human HIV.
XX
XX Group O human immune deficiency virus; HIV; detection; infection.
XX
XX Synthetic.
XX
XX Immune deficiency virus.
XX
XX WO9845323-A1.
XX
XX 15-OCT-1998.
XX
XX 06-APR-1998; 98WO-FR00691.
XX
XX 24-FEB-1998; 98FR-0002212.
XX
XX 09-APR-1997; 97FR-0004356.
XX
XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.
XX
XX Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;
XX
XX WPI; 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 43; 55pp; French.
XX
XX AAW80459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O
XX human immune deficiency virus (HIV).
XX
XX Sequence 22 AA;

Query Match 96.7%; Score 88; DB 19; Length 22;
XX Best Local Similarity 93.8%; Pred. No. 3.7e-06;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTS 16
   ||:|||||
Db 1 LLSWGCKGRIVCYTS 16

RESULT 7
AAW80473
ID AAW80473 standard; peptide; 28 AA.
XX
XX AAW80473;
XX
XX 28-JAN-1999 (first entry)
XX

```

XX Peptide derived from a conserved sequence of group O human HIV.
 DE
 XX
 XX Group O human immune deficiency virus; HIV; detection; infection.
 KW
 XX Synthetic.
 OS
 XX Immune deficiency virus.
 OS
 XX WO9845323-A1.
 PN
 XX
 XX 15-OCT-1998.
 PD
 XX
 XX 06-APR-1998; 98WO-FR00691.
 PF
 XX
 XX 24-FEB-1998; 98FR-0002212.
 PR
 XX 09-APR-1997; 97FR-0004356.
 PR
 XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 PA
 XX
 XX Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY,
 WPI; 1998-583190/49.

XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX
 XX Claim 6; Page 44; 55pp; French.
 PS
 XX AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 28 AA;

Query Match 96.7%; Score 88; DB 19; Length 28;
 Best Local Similarity 93.8%; Pred. No. 4.6e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRVLCYTS 16
 ||:|||||
 DB 12 LLSWGCKGRVLCYTS 27

RESULT 8

AA12212
 AAB12212 standard; peptide; 33 AA.

AC AAB12212;
 XX
 DT 10-NOV-2000 (first entry)
 XX
 DE Partial sequence of HIV-1 strain BCF13 gp41 immunodominant region.
 XX
 KW HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
 KW acquired immunodeficiency syndrome; group O HIV; gp41; BCF13.
 XX
 OS Human immunodeficiency virus type 1.
 OS
 XX EPI013766-A2.
 PN
 XX 28-JUN-2000.
 PD
 XX 29-NOV-1999; 99EP-0309491.
 PF
 XX 30-NOV-1998; 98US-0110292.
 PR 08-FEB-1999; 99US-0119138.
 PR 04-NOV-1999; 99US-0433428.
 XX
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 XX

PI De Lays R, Zheng J;
 XX
 XX WPI; 2000-402205/35.
 DR

PT New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 XX virus group O antibodies -
 XX

Example 1; Fig 1; 52pp; English.

CC The present sequence is a partial gp41 protein of Human Immunodeficiency
 CC Virus Type 1 (HIV-1) strain BCF13. HIV is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of
 CC antibodies produced in response to HIV infection. BCF13 is a member of
 CC HIV group O (outlier). The present sequence is the immunodominant region
 CC of gp41. This sequence was used in a sequence homology alignment,
 CC which in turn was used to derive a consensus sequence peptide: peptide
 CC 147 (AAB12254).
 XX

SQ Sequence 33 AA;

Query Match 96.7%; Score 88; DB 21; Length 33;
 Best Local Similarity 93.8%; Pred. No. 5.4e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRVLCYTS 16
 ||:|||||
 DB 14 LLSWGCKGRVLCYTS 29

RESULT 9
 AAB12231
 AAB12231 standard; peptide; 33 AA.

AC AAB12231;

DT 10-NOV-2000 (first entry)

DE Partial sequence of HIV-1 strain MAN gp41 immunodominant region.

KW HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
 KW acquired immunodeficiency syndrome; group O HIV; gp41; MAN.
 XX

OS Human immunodeficiency virus type 1.

EPI013766-A2.

PN 28-JUN-2000.

PF 29-NOV-1999; 99EP-0309491.

PR 30-NOV-1998; 98US-0110292.

PR 08-FEB-1999; 99US-0119138.

PR 04-NOV-1999; 99US-0433428.

PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

PI De Lays R, Zheng J;

DR WPI; 2000-402205/35.

PT New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 XX virus group O antibodies -
 XX

Example 1; Fig 1; 52pp; English.

CC The present sequence is a partial gp41 protein of Human Immunodeficiency
 CC Virus Type 1 (HIV-1) strain MAN. HIV is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of
 CC antibodies produced in response to HIV infection. MAN is a member of

CC HIV group O (outlier). The present sequence is the immunodominant region
CC of gp1. This sequence was used in a sequence homology alignment,
CC which in turn was used to derive a consensus sequence peptide: peptide
CC 147 (AAB12254).

XX
XX
SQ Sequence 33 AA;

Query Match 96.7%; Score 88; DB 21; Length 33;
Best Local Similarity 93.8%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCYTS 16
||:|||||
Db 14 LLSWGCKGRIVCYTS 29

RESULT 10
AAM07346
ID AAM07346 standard; peptide; 40 AA.

AAM07346;
03-JUN-1997 (first entry)

DE Partial sequence of gp1 from HIV-1 gp. O strain BCF07 (MAN).

XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
XX C2V3-env; gp1; gag; retrovirus; strain; gp120; hypervariable loop;
XX primer; hybridisation; amplification; PCR; polymerase chain reaction;
XX immunogen; antibody.

OS Human immunodeficiency virus type 1.
XX
XX WO9627013-A1.
XX
XX 06-SEP-1996.
XX
XX 26-FEB-1996; 96WO-FR00294.
XX
XX 27-FEB-1995; 95FR-0002236.
XX
XX
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;
XX MPI; 1996-412779/41.
XX N-PSDB; AAT44922.

PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and
PT antibodies - useful for diagnosis, screening and typing, or as
PT immunogens

XX
XX PS Claim 12; Page 34; 71pp; French.

CC Human immunodeficiency virus type 1 (HIV-1) strains are currently
CC divided into 2 major groups based on the nucleotide sequences of the
CC envelope gene (env): group M containing sub-groups A-G, and group O
CC containing the strains AN70 and MWP5180. The invention relates to the
CC discovery of several new strains of HIV-1 which can be placed in group O,
CC based on the partial sequences of the C2V3-env, gp1 and gag genes (see
CC AAT44907-39 and AAM07329-64). The novel strains have been deposited as
CC retroviruses CNCM 1-1544 (BCF02 (ESS)), 1543 (BCF01 (PAN)), 1546 (BCF07
CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
CC presented here is from the strain BCF07 (MAN) and corresponds to a
CC fragment of the gp1 protein encoded by the env gene. The nucleic acids
CC can be used to detect gp. O HIV-1 strains by hybridisation or (as
CC primers) by gene amplification, also for screening and typing of such
CC strains. Peptides encoded by the nucleic acids can be used as immunogens
CC to raise Ab for detecting gp. O HIV-1.

XX
XX Sequence 40 AA;

Query Match 96.7%; Score 88; DB 17; Length 40;
Best Local Similarity 93.8%; Pred. No. 6.5e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCYTS 16
||:|||||
Db 19 LLSWGCKGRIVCYTS 34

RESULT 11
AAM07352
ID AAM07352 standard; peptide; 40 AA.

AAM07352;
03-JUN-1997 (first entry)

DE Partial sequence of gp1 from HIV-1 gp. O strain BCF13.

XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
XX C2V3-env; gp1; gag; retrovirus; strain; gp120; hypervariable loop;
XX primer; hybridisation; amplification; PCR; polymerase chain reaction;
XX immunogen; antibody.

OS Human immunodeficiency virus type 1.
XX
XX WO9627013-A1.
XX
XX 06-SEP-1996.
XX
XX 26-FEB-1996; 96WO-FR00294.
XX
XX 27-FEB-1995; 95FR-0002236.
XX
XX
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;
XX MPI; 1996-412779/41.
XX

PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and
PT antibodies - useful for diagnosis, screening and typing, or as
PT immunogens

XX
XX PS Claim 12; Page 46; 71pp; French.

CC Human immunodeficiency virus type 1 (HIV-1) strains are currently
CC divided into 2 major groups based on the nucleotide sequences of the
CC envelope gene (env): group M containing sub-groups A-G, and group O
CC containing the strains AN70 and MWP5180. The invention relates to the
CC discovery of several new strains of HIV-1 which can be placed in group O,
CC based on the partial sequences of the C2V3-env, gp1 and gag genes (see
CC AAT44907-39 and AAM07329-64). The novel strains have been deposited as
CC retroviruses CNCM 1-1544 (BCF02 (ESS)), 1543 (BCF01 (PAN)), 1546 (BCF07
CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
CC presented here is from the strain BCF13 and corresponds to a fragment of
CC the gp1 protein encoded by the env gene. The nucleic acids can be used
CC to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene
CC amplification, also for screening and typing of such strains. Peptides
CC encoded by the nucleic acids can be used as immunogens to raise Ab for
CC detecting gp. O HIV-1.

XX
XX Sequence 40 AA;

Query Match 96.7%; Score 88; DB 17; Length 40;
Best Local Similarity 93.8%; Pred. No. 6.5e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCYTS 16
||:|||||
Db 19 LLSWGCKGRIVCYTS 34

PT antibodies - useful for diagnosis, screening and typing, or as
 immunogens

PS Claim 12; Page 33; 71pp; French.

XX Human immunodeficiency virus type 1 (HIV-1) strains are currently
 CC divided into 2 major groups based on the nucleotide sequences of the
 CC envelop gene (env): group M containing sub-groups A-G, and group O
 CC containing the strains ANR70 and MWP5180. The invention relates to the
 CC discovery of several new strains of HIV-1 which can be placed in group O,
 CC based on the partial sequences of the C23-env, gp41 and gag genes (see
 CC AAT44907-39 and AAW07329-64). The novel strains have been deposited as
 CC retroviruses CCM 1-1544 (BCF02 (ESS)), 1543 (BCF01 (PAN)), 1546 (BCF07
 CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
 CC presented here is from the strain BCF02 (ESS) and corresponds to a
 CC fragment of the gp41 protein encoded by the env gene. The nucleic acids
 CC can be used to detect gp. O HIV-1 strains by hybridisation or (as
 CC primers) by gene amplification, also for screening and typing of such
 CC strains. Peptides encoded by the nucleic acids can be used as immunogens
 CC to raise Ab for detecting gp. O HIV-1.

Sequence 40 AA;

Query Match 94.5%; Score 86; DB 17; Length 40;

Best Local Similarity 87.5%; Pred. No. 1.3e-05;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTS 16

Db 19 LLSWGCKGRIVCYTS 34

RESULT 15

AAW80469

ID AAW80469 standard; peptide; 32 AA.

XX AAW80469;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.

OS Immune deficiency virus.

XX WO9845323-A1.

15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

XX 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

DR WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 human immune deficiency virus of group O

XX Claim 6; Page 44; 55pp; French.

XX AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).

XX Sequence 32 AA;

Query Match 93.4%; Score 85; DB 19; Length 32;

Best Local Similarity 87.5%; Pred. No. 1.4e-05;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTS 16

Db 11 LLSWGCKGRIVCYTS 26

Search completed: May 29, 2003, 10:36:22
 Job time : 21.3333 secs

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OM protein - protein search, using 5w model

Run on: May 29, 2003, 10:33:36 ; Search time 7.2381 Seconds
(without alignments)
65.040 Million cell updates/sec

Title: US-09-147-362A-9
Perfect score: 91
Sequence: 1 LLSWGCKGRIVCYTS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
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2	88	96.7	33	4	US-09-433-428D-25
3	88	96.7	40	3	US-08-894-699-39
4	88	96.7	40	3	US-08-894-699-68
5	88	96.7	40	4	US-09-444-410-39
6	88	96.7	40	4	US-09-444-410-68
7	86	94.5	33	4	US-09-433-428D-30
8	86	94.5	40	3	US-08-894-699-36
9	86	94.5	40	4	US-09-444-410-36
10	85	93.4	33	4	US-09-433-428D-20
11	85	93.4	40	3	US-08-894-699-41
12	85	93.4	40	4	US-09-444-410-41
13	82	90.1	23	4	US-09-433-428D-68
14	82	90.1	33	4	US-09-433-428D-1
15	82	90.1	33	4	US-09-433-428D-7
16	82	90.1	33	4	US-09-433-428D-15
17	82	90.1	37	4	US-08-817-441-86
18	82	90.1	41	3	US-08-894-699-65
19	82	90.1	41	4	US-09-444-410-69
20	82	90.1	42	4	US-08-894-699-66
21	82	90.1	42	4	US-09-444-410-66
22	82	90.1	200	4	US-08-965-056-104
23	82	90.1	23	4	US-09-433-428D-59
24	81	89.0	23	4	US-09-433-428D-60
25	81	89.0	23	4	US-09-433-428D-61
26	81	89.0	23	4	US-09-433-428D-61
27	81	89.0	28	4	US-09-433-428D-62

28	81	89.0	30	4	US-09-433-428D-63	Sequence 63, Appl
29	81	89.0	30	4	US-09-433-428D-69	Sequence 69, Appl
30	81	89.0	33	4	US-09-433-428D-5	Sequence 5, Appl
31	81	89.0	33	4	US-09-433-428D-8	Sequence 8, Appl
32	81	89.0	33	4	US-09-433-428D-14	Sequence 14, Appl
33	81	89.0	33	4	US-09-433-428D-16	Sequence 16, Appl
34	81	89.0	33	4	US-09-433-428D-29	Sequence 29, Appl
35	81	89.0	35	4	US-09-433-428D-64	Sequence 64, Appl
36	81	89.0	41	3	US-08-894-699-67	Sequence 67, Appl
37	81	89.0	41	4	US-09-444-410-67	Sequence 67, Appl
38	81	89.0	149	4	US-09-433-428D-67	Sequence 67, Appl
39	81	89.0	215	2	US-08-912-129A-58	Sequence 58, Appl
40	81	89.0	220	4	US-09-433-428D-66	Sequence 66, Appl
41	81	89.0	245	2	US-08-912-129A-48	Sequence 48, Appl
42	81	89.0	368	4	US-09-433-428D-58	Sequence 58, Appl
43	81	89.0	373	2	US-08-912-129A-52	Sequence 52, Appl
44	81	89.0	439	2	US-09-433-428D-57	Sequence 57, Appl
45	81	89.0	460	2	US-08-912-129A-60	Sequence 60, Appl

ALIGNMENTS

```

RESULT 1
US-09-433-428D-6
; Sequence 6, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Ley, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-6

Query Match          96.7% Score 88; DB 4; Length 33;
Best Local Similarity 93.8% Pred. No. 4.3e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLSWGCKGRIVCYTS 16
Db      14 LLSWGCKGRIVCYTS 29

RESULT 2
US-09-433-428D-25
; Sequence 25, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Ley, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 25
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-25

Query Match          96.7% Score 88; DB 4; Length 33;
Best Local Similarity 93.8% Pred. No. 4.3e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

CY 1 LLSWGCKGRVLYCYTS 16
||:|||||
Db 14 LLSWGCKGRVLYCYTS 29

RESULT 3

US-08-894-699-39
; Sequence 39, Application US/08894699
; Patent No. 6030769

GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-39

Query Match 96.7%; Score 88; DB 3; Length 40;
Best Local Similarity 93.8%; Pred. No. 5.2e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 LLSWGCKGRVLYCYTS 16
||:|||||
Db 19 LLSWGCKGRVLYCYTS 34

RESULT 4

US-08-894-699-68
; Sequence 68, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-68

Query Match 96.7%; Score 88; DB 3; Length 40;
Best Local Similarity 93.8%; Pred. No. 5.2e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 LLSWGCKGRVLYCYTS 16
||:|||||
Db 19 LLSWGCKGRVLYCYTS 34

RESULT 5
US-09-444-410-39
; Sequence 39, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-39

Query Match 96.7%; Score 88; DB 4; Length 40;
Best Local Similarity 93.8%; Pred. No. 5.2e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

OY 1 LLSWGCKGRIVCYTS 16
||:|||||||
Db 19 LLSWGCKGRIVCYTS 34

RESULT 6
US-09-444-410-68
Sequence 68, Application US/09444410
Patent No. 6270975

GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEST-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P. C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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1      CURRENT APPLICATION DATA:
2      APPLICATION NUMBER:    US/09/444,410
3      FILING DATE:
4      CLASSIFICATION:
5      PRIOR APPLICATION DATA:
6      APPLICATION NUMBER:    08/894,699
7      FILING DATE:
8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER:    FR 95/02236
10     FILING DATE:    27-FEB-1995
11     ATTORNEY/AGENT INFORMATION:
12     NAME:    OBOLON, NORMAN F.
13     REGISTRATION NUMBER:    24,614
14     REFERENCE/DOCKET NUMBER:    0354-0020-0PCT
15     TELECOMMUNICATION INFORMATION:
16     TELEPHONE:    703-413-3000
17     TELEFAX:    703-413-2220
18     INFORMATION FOR SEQ ID NO:    68:
19     SEQUENCE CHARACTERISTICS:
20     LENGTH:    40 amino acids
21     TYPE:    amino acid
22     STRANDEDNESS:    single
23     TOPOLOGY:    linear
24     MOLECULE TYPE:    peptide
25     US-09-444-410-68

```

Query Match	96.7%	Score 88;	DB 4;	Length 40;
Best Local Similarity	93.8%	Pred. No. 5.2e-07;		
Matches 15;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      1  LLSSWGCKGRLVCYTS  16
          ||:|||||
Db      19  LLNSWGCKGRLVCYTS  34

```

```

1  RESULT 7
2  US-09-433-428D-30
3  : Sequence 30, Application US/09433428D
4  : Patent No. 6149910
5  : GENERAL INFORMATION:
6  :
7  : APPLICANT: De leys, Robert J.
8  : APPLICANT: Zheng, Jian
9  : TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
10 : FILE REFERENCE: CDS-207
11 : CURRENT APPLICATION NUMBER: US/09/433.428D
12 : CURRENT FILING DATE: 1999-11-04
13 : NUMBER OF SEQ ID NOS: 70
14 : SOFTWARE: PatentIn Ver. 2.0
15 : SEQ ID NO: 30
16 : LENGTH: 33
17 :
18 : TYPE: PRT
19 :
20 : ORGANISM: Human immunodeficiency virus type 1
21 : US-09-433-428D-30

```

```

Query Match      94.5%; Score 86; DB 4; Length 33;
Best Local Similarity 87.5%; Pred. No. 8.7e-07;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLSWGCKGRLLNYCTYS 16
          |||..|||..|||
Db      14 LLSWGCKGRIVCYTS 29

```

RESULT 8
 US-08-894-699-36
 ; Sequence 36, Application US/08894699
 ; Patent No. 6030769
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMON, FRANCOIS
 ; APPLICANT: SARGOSTI, SENTOB
 ; APPLICANT: LOUISSEST-ADJAKA, IBETISSAM
 ; APPLICANT: LY THOI-DONG
 ; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C. OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-36

Query Match 94.5%; Score 86; DB 3; Length 40;
Best Local Similarity 87.5%; Pred. No. 1e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTS 16
||:|||||:|||||
19 LLSWGCKGRIVCYTS 34

RESULT 9
US-09-444-410-36
Sequence 36, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-36

Query Match 94.5%; Score 86; DB 4; Length 40;
Best Local Similarity 87.5%; Pred. No. 1e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
||:|||||:|||||
DB 19 LLSWGCKGRIVCYTS 34

RESULT 10
US-09-433-428D-20
Sequence 20, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Ley, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 33
TYPE: PPT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-20

Query Match 93.4%; Score 85; DB 4; Length 33;
Best Local Similarity 93.8%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
||:|||||:|||||
DB 14 LLSWGCKGRIVCYTS 29

RESULT 11
US-08-894-699-41
Sequence 41, Application US/08894699
Patent No. 6030769

GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEST-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
Query Match 93.4%; Score 85; DB 3; Length 40;
Best Local Similarity 93.8%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LLSWGCKGRIVCYTS 16
DB 19 LLSWGCKGRIVCYTS 34
RESULT 12
US-09-444-410-41
Sequence 41, Application US/09444410
Patent No. 6270975
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSEST-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 08/894,699
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/894,699
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-41
Query Match 93.4%; Score 85; DB 4; Length 40;
Best Local Similarity 93.8%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LLSWGCKGRIVCYTS 16
DB 19 LLSWGCKGRIVCYTS 34
RESULT 13
US-09-433-428D-68
Sequence 68, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leye, Robert J.
APPLICANT: Zheng, Jien
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentn Ver. 2.0
SEQ ID NO 68
LENGTH: 23
TYPE: PPT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-68
Query Match 90.1%; Score 82; DB 4; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.5e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 LLSWGCKGRIVCYTS 16
DB 4 LLSWGCKGRIVCYTS 19

RESULT 14

US-09-433-428D-1
 ; Sequence 1, Application US/09433428D
 ; Patent No. 6149910
 ; GENERAL INFORMATION:
 ; APPLICANT: De Ley, Robert J.
 ; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
 ; FILE REFERENCE: CDS-207
 ; CURRENT APPLICATION NUMBER: US/09/433,428D
 ; CURRENT FILING DATE: 1999-11-04
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 ; 09-433-428D-1

Query Match

Best Local Similarity 90.1%; Score 82; DB 4; Length 33;
 Best Local Similarity 87.5%; Pred. No. 3.5e-06;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCYTS 16

Db 14 LLSWGCKGRLVCYTS 29

RESULT 15

US-09-433-428D-4
 ; Sequence 4, Application US/09433428D
 ; Patent No. 6149910
 ; GENERAL INFORMATION:
 ; APPLICANT: De Ley, Robert J.
 ; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
 ; FILE REFERENCE: CDS-207
 ; CURRENT APPLICATION NUMBER: US/09/433,428D
 ; CURRENT FILING DATE: 1999-11-04
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 ; 09-433-428D-4

Query Match

Best Local Similarity 90.1%; Score 82; DB 4; Length 33;
 Best Local Similarity 87.5%; Pred. No. 3.5e-06;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCYTS 16

Db 14 LLSWGCKGRLVCYTS 29

Search completed: May 29, 2003, 10:41:28
 Job time : 7.2381 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:39:21 ; Search time 13.8413 Seconds
(without alignments)
117.011 Million cell updates/sec

Title: US-09-147-362A-9
Perfect score: 91
Sequence: 1 LLSWGCKGRVCTYS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

1 number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	90.1	37	9	US-10-026-741-86
2	82	90.1	200	10	US-09-854-816-104
3	81	89.0	215	1	US-08-911-824-58
4	81	89.0	245	1	US-08-911-824-48
5	81	89.0	281	1	US-08-911-824-100
6	81	89.0	373	1	US-08-911-824-52
7	81	89.0	460	1	US-08-911-824-60
8	81	89.0	488	1	US-08-911-824-95
9	81	89.0	490	1	US-08-911-824-50
10	81	89.0	526	1	US-08-911-824-97
11	81	89.0	618	1	US-08-911-824-54
12	81	89.0	706	1	US-08-911-824-93
13	81	89.0	736	1	US-08-911-824-91
14	81	89.0	873	1	US-08-911-824-61
15	79	86.8	22	9	US-10-059-271-6
16	79	86.8	22	9	US-10-059-271-8
17	79	86.8	254	9	US-10-059-271-82
18	79	86.8	256	9	US-10-059-271-97
19	79	86.8	1231	9	US-10-059-271-94

20	78	85.7	213	10	US-09-854-816-103	Sequence 103, App
21	76	83.5	22	9	US-10-059-271-7	Sequence 7, Appl
22	75	82.4	35	9	US-10-026-741-101	Sequence 101, App
23	75	82.4	37	9	US-10-026-741-7	Sequence 7, Appl
24	75	82.4	37	9	US-10-026-741-90	Sequence 90, Appl
25	75	82.4	351	9	US-10-026-741-47	Sequence 47, Appl
26	75	82.4	877	9	US-10-026-741-102	Sequence 102, App
27	74	81.3	23	9	US-09-388-847-4	Sequence 4, Appl
28	74	81.3	23	12	US-10-000-321-2	Sequence 2, Appl
29	74	81.3	35	9	US-09-886-156-62	Sequence 62, Appl
30	74	81.3	35	9	US-09-886-150-62	Sequence 62, Appl
31	74	81.3	35	9	US-09-886-149-62	Sequence 62, Appl
32	74	81.3	35	9	US-09-886-159-62	Sequence 62, Appl
33	74	81.3	37	9	US-10-026-741-88	Sequence 88, Appl
34	74	81.3	146	12	US-10-000-321-10	Sequence 10, Appl
35	74	81.3	204	10	US-09-854-816-105	Sequence 105, App
36	74	81.3	351	9	US-09-886-156-46	Sequence 46, Appl
37	74	81.3	351	9	US-09-886-150-46	Sequence 46, Appl
38	74	81.3	351	9	US-09-886-149-46	Sequence 46, Appl
39	74	81.3	351	9	US-09-886-159-46	Sequence 46, Appl
40	70	76.9	24	9	US-10-026-741-34	Sequence 34, Appl
41	70	76.9	29	9	US-10-026-741-33	Sequence 33, Appl
42	70	76.9	37	9	US-10-026-741-94	Sequence 94, Appl
43	70	76.9	104	9	US-10-026-741-100	Sequence 100, App
44	70	76.9	221	9	US-10-059-271-84	Sequence 84, Appl
45	68	74.7	22	9	US-10-059-271-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-026-741-86
; Sequence 86, Application US/10026741
; Publication No. US2003049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
QUILLIENT, CAROLINE
GUETARD, DENISE
MONTAGNER, LUC
DONON DE SAINT-MARTIN, JACELINE
COHEN, JAOUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegun, Henderson, Farabow, Garrett &
Dunnet, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM-TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/917,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-026-741-86

Query Match 90.1%; Score 82; DB 9; Length 37;
Best Local Similarity 87.5%; Pred. No. 1.7e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTS 16
||| ||||| |||||
14 LLSWGCKGRIVCYTS 29

Db

RESULT 2
US-09-854-816-104
Sequence 104, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
U. Kevin Judice
Robert S. McDowell
J. Christopher Pheasant
Melissa A. Starovassnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-854-816-104

Query Match 90.1%; Score 82; DB 10; Length 200;
Best Local Similarity 87.5%; Pred. No. 7.6e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTS 16
||| ||||| |||||
126 LLSWGCKGRIVCYTS 141

Db

RESULT 3
US-08-911-824-58
Sequence 58, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 58
LENGTH: 215
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-8PL
US-08-911-824-58

Query Match 89.0%; Score 81; DB 1; Length 215;
Best Local Similarity 81.2%; Pred. No. 0.00011;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTS 16
||| ||||| |||||
127 LLSWGCKGRIVCYTS 142

Db

RESULT 4
US-08-911-824-48
Sequence 48, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 48
LENGTH: 245
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-9PL
US-08-911-824-48

Query Match 89.0%; Score 81; DB 1; Length 245;

Best Local Similarity 81.2%; Pred. No. 0.00013;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTS 16
Db 127 LNLWGCKGRIVCYTS 142

RESULT 5

US-08-911-824-120
Sequence 120, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.

TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165, US, 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 120
LENGTH: 281
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:

OTHER INFORMATION: Encodes recombinant protein pGO-15PL
US-08-911-824-120

Query Match 89.0%; Score 81; DB 1; Length 281;
Best Local Similarity 81.2%; Pred. No. 0.00014;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTS 16
Db 127 LNLWGCKGRIVCYTS 142

RESULT 6

US-08-911-824-52
Sequence 52, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.

TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165, US, 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 52
LENGTH: 373
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:

OTHER INFORMATION: Encodes recombinant protein pGO-11PL
US-08-911-824-52

Query Match 89.0%; Score 81; DB 1; Length 373;
Best Local Similarity 81.2%; Pred. No. 0.00018;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTS 16
Db 127 LNLWGCKGRIVCYTS 142

RESULT 7

US-08-911-824-60
Sequence 60, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.

TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165, US, 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 460
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:

OTHER INFORMATION: Encodes recombinant protein pGO-8CKS
US-08-911-824-60

Query Match 89.0%; Score 81; DB 1; Length 460;
Best Local Similarity 81.2%; Pred. No. 0.00022;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTS 16
Db 372 LNLWGCKGRIVCYTS 387

RESULT 8

US-08-911-824-95
Sequence 95, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.

TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165, US, 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 95
LENGTH: 488
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:

OTHER INFORMATION: Encodes recombinant protein pGO-14PL
US-08-911-824-95

Query Match 89.0%; Score 81; DB 1; Length 488;
Best Local Similarity 81.2%; Pred. No. 0.00023;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
||:|||||:
Db 127 LNLWGCKGRIVCYTS 142

RESULT 9

US-08-911-824-50
; Sequence 50, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-9CKS
US-08-911-824-50

Query Match 89.0%; Score 81; DB 1; Length 490;
Best Local Similarity 81.2%; Pred. No. 0.00023;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
||:|||||:
Db 372 LNLWGCKGRIVCYTS 387

RESULT 10

US-08-911-824-97
; Sequence 97, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-15CKS
US-08-911-824-97

Query Match 89.0%; Score 81; DB 1; Length 526;
Best Local Similarity 81.2%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
||:|||||:
Db 372 LNLWGCKGRIVCYTS 387

RESULT 11

US-08-911-824-54
; Sequence 54, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-11CKS
US-08-911-824-54

Query Match 89.0%; Score 81; DB 1; Length 618;
Best Local Similarity 81.2%; Pred. No. 0.00028;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
||:|||||:
Db 372 LNLWGCKGRIVCYTS 387

RESULT 12

US-08-911-824-93
; Sequence 93, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165.US.O1
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-13CKS
US-08-911-824-93

Query Match 89.0%; Score 81; DB 1; Length 706;
Best Local Similarity 81.2%; Pred. No. 0.00032;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 618 L1N1MGCKGR1CYTS 633

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RESULT 13
US-08-911-824-91
; Sequence 91, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Encodes recombinant protein pCO-12CKS
US-08-911-824-91

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Query Match 89.0%; Score 81; DB 1; Length 736;
Best Local Similarity 81.2%; Pred. No. 0.00033;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Cy 1 L1SSWGCKGR1CYTS 16
Db 618 L1N1MGCKGR1CYTS 633

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RESULT 14
US-08-911-824-61
; Sequence 61, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 873
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: HIV-1 Group O isolate HAM12
US-08-911-824-61

```

```

Query Match 89.0%; Score 81; DB 1; Length 873;
Best Local Similarity 81.2%; Pred. No. 0.00038;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Cy 1 L1SSWGCKGR1CYTS 16
Db 618 L1N1MGCKGR1CYTS 633

```

Db 601 L1N1MGCKGR1CYTS 616

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RESULT 15
US-10-059-271-6
; Sequence 6, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPRX, HEINRICH
; APPLICANT: BUDD, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-6

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Query Match 86.8%; Score 79; DB 9; Length 22;
Best Local Similarity 81.2%; Pred. No. 3.1e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Cy 1 L1SSWGCKGR1CYTS 16
Db 7 L1N1MGCKGR1CYTN 22

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Job time : 14.843 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:06 ; Search time 7.87302 Seconds
(without alignments)
195.370 Million cell updates/sec

Title: US-09-147-362A-9

Perfect score: 91

Sequence: 1 LLSWGCKGRLLVCYTS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	90.1	863	2 A53034	gag polyprotein -
2	75	82.4	877	2 S49197	envelope protein p
3	70	76.9	104	2 S52930	GP41 ENV protein
4	63	69.2	357	2 S21990	envelope protein g
5	63	69.2	358	2 S22002	envelope protein g
6	63	69.2	854	1 VCLJST	env polyprotein pr
7	62	68.1	358	2 S22000	envelope protein g
8	62	68.1	358	2 S70417	envelope protein g
9	62	65.9	357	2 S22006	envelope protein g
10	60	65.9	357	2 S21994	envelope protein g
11	60	65.9	357	2 S22004	envelope protein g
12	60	65.9	357	2 S21996	envelope protein g
13	60	65.9	357	2 S21992	envelope protein g
14	60	65.9	358	2 S21998	envelope protein g
15	60	65.9	443	2 C41621	env polyprotein p
16	60	65.9	443	2 A41621	env polyprotein M
17	60	65.9	454	2 B41621	env polyprotein D
18	60	65.9	843	1 H44001	env polyprotein pr
19	60	65.9	847	1 T09448	envelope glycoprot
20	60	65.9	847	2 S13289	env protein - huma
21	60	65.9	852	1 VCLJBR	env polyprotein -
22	60	65.9	852	2 T12016	envelope glycoprot
23	60	65.9	853	2 S54384	envelope glycoprot
24	60	65.9	853	2 S13288	env protein - huma
25	60	65.9	855	1 VCLJAZ	env polyprotein pr
26	60	65.9	855	1 VCLJZR	env polyprotein pr
27	60	65.9	856	1 VCLJVL	env polyprotein pr
28	60	65.9	856	1 VCLJVL	env polyprotein pr
29	60	65.9	856	1 VCLJVM	env polyprotein pr

30	60	65.9	859	1 VCLJVN	env polyprotein pr
31	60	65.9	861	1 VCLJLV	env polyprotein pr
32	60	65.9	861	1 VCLJSC	env polyprotein pr
33	60	65.9	868	1 VCLJH4	env polyprotein -
34	59	64.8	855	2 A45713	Env transmembrane
35	58	63.7	859	1 VCLJST	env polyprotein pr
36	57	62.6	786	2 S28084	env polyprotein -
37	57	62.6	856	1 A44963	env polyprotein pr
38	56	61.5	846	1 VCLJND	env polyprotein -
39	55	60.4	151	2 S30458	env protein - huma
40	55	60.4	151	2 S30459	env protein - huma
41	55	60.4	151	2 S30448	env protein - huma
42	55	60.4	151	2 S30453	env protein - huma
43	55	60.4	151	2 S30452	env protein - huma
44	55	60.4	151	2 S30450	env protein - huma
45	55	60.4	151	2 S30451	env protein - huma

ALIGNMENTS

RESULT 1
A53034
gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: A53034
J:Vand. 68, 1586-1596, 1994
R:Vanden Haesevelde, M.; Decourt, J.L.; De Lays, R.J.; Vanderborght, B.; van der Groen, J.
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African hu
A:Reference number: A53034; MUID:94149849; PMID:8107220
A:Accession: A53034
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-863 <VAN>
A:Cross-references: GB:L02587
C:Superfamily: type B retrovirus env polyprotein
C:Keywords: polyprotein

Query Match 90.1%; Score 82; DB 2; Length 863;
Best Local Similarity 87.5%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRLLVCYTS 16
DB 594 LLSWGCKGRLLVCYTS 609

RESULT 2
S49197
envelope protein precursor - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
C:Accession: S49197
R:Charneau, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chameret, S.; Cohen, J.; Remy, J.
submitted to the EMBL Data Library, July 1994
A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi
A:Reference number: S49197
A:Accession: S49197
A:Molecule type: DNA
A:Residues: 1-877 <CH>
A:Cross-references: EMBL:X80020; NID:G510516; PIDN:CA56323.1; PID:G510517
A:Experimental source: isolate VAV
C:Superfamily: type B retrovirus env polyprotein
C:Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-535/Product: coat protein gp120 #status predicted <CP1>
F:536-877/Product: coat protein gp41 #status predicted <CP2>
F:698-716/Domain: transmembrane #status predicted <TMN>
F:59, 88, 139, 148, 159, 184, 188, 198, 230, 242, 263, 270, 272, 292, 302, 333, 345, 357, 367, 396, 404,
Query Match 82.4%; Score 75; DB 2; Length 877;
Best Local Similarity 75.0%; Pred. No. 0.001;

C;Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
 C/Accession: S22000
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
 A:Reference number: S21990
 A/Accession: S22000
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-358 <STB>
 A/Cross-references: EMBL:X61351
 C/Superfamily: type E retrovirus env polypeptide

Query Match 68.1%; Score 62; DB 2; Length 358;
 Best Local Similarity 66.7%; Pred. No. 0.048;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYT 15
 94 LLSWGCKGRIVCYT 108

RESULT 8
 S70417
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Variety: patient 3B
 C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
 C/Accession: S70417
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 A/ID: Res. Hum. Retroviruses 8, 53-59, 1992
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR
 A/Reference number: S70417; MUID:92144209; PMID:1736940
 A/Accession: S70417
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-358 <STB>
 A/Cross-references: EMBL:X61351; NID:G60184; PID:CAA43614.1; PID:G60185
 C/Superfamily: type E retrovirus env polypeptide

Query Match 68.1%; Score 62; DB 2; Length 358;
 Best Local Similarity 66.7%; Pred. No. 0.048;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYT 15
 94 LLSWGCKGRIVCYT 108

RESULT 9
 S22006
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
 C/Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C/Accession: S70420; S22006
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 A/ID: Res. Hum. Retroviruses 8, 53-59, 1992
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR
 A/Reference number: S70417; MUID:92144209; PMID:1736940
 A/Accession: S70420
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-357 <ST2>
 A/Cross-references: EMBL:X61354; NID:G60190; PID:CAA43620.1; PID:G60191
 A/Experimental source: patient L
 A/Note: submitted to the EMBL Data Library, July 1991
 C/Superfamily: type E retrovirus env polypeptide

Query Match 65.9%; Score 60; DB 2; Length 357;
 Best Local Similarity 56.2%; Pred. No. 0.096;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYT 16
 94 LLSWGCKGRIVCYT 108

Db 93 LLSWGCKGRIVCYT 108

RESULT 10
 S21994
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Variety: isolate 27B
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C/Accession: S21994; S70421
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 A/ID: Res. Hum. Retroviruses 8, 53-59, 1992
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR
 A/Reference number: S21990
 A/Accession: S21994
 A/Molecule type: DNA
 A/Residues: 1-357 <STB1>
 A/Cross-references: EMBL:X61355; NID:G60179; PID:CAA43622.1; PID:G60180
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 A/ID: Res. Hum. Retroviruses 8, 53-59, 1992
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR
 A/Reference number: S70417; MUID:92144209; PMID:1736940
 A/Accession: S70421
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-140, 'X', 142-312, 'X', 314-357 <STB2>
 A/Cross-references: EMBL:X61355; NID:G60179
 C/Superfamily: type E retrovirus env polypeptide

Query Match 65.9%; Score 60; DB 2; Length 357;
 Best Local Similarity 56.2%; Pred. No. 0.096;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYT 16
 93 LLSWGCKGRIVCYT 108

RESULT 11
 S22004
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Variety: isolate 4B
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C/Accession: S22004; S70419
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 A/ID: Res. Hum. Retroviruses 8, 53-59, 1992
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR
 A/Reference number: S21990
 A/Accession: S22004
 A/Molecule type: DNA
 A/Residues: 1-357 <STB1>
 A/Cross-references: EMBL:X61353; NID:G60188; PID:CAA43618.1; PID:G60189
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 A/ID: Res. Hum. Retroviruses 8, 53-59, 1992
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR
 A/Reference number: S70417; MUID:92144209; PMID:1736940
 A/Accession: S70419
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-292, 'X', 294-357 <STB2>
 A/Cross-references: EMBL:X61353; NID:G60188
 C/Superfamily: type E retrovirus env polypeptide

Query Match 65.9%; Score 60; DB 2; Length 357;
 Best Local Similarity 56.2%; Pred. No. 0.096;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYT 16
 93 LLSWGCKGRIVCYT 108

RESULT 12

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S70422; S21996

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70422

A:Status: preliminary

A:Accession: S70422

A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129

A:Experimental source: patient 27L

A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polyprotein

Query Match 65.9%; Score 60; DB 2; Length 357;

Best Local Similarity 56.2%; Pred. No. 0.096;

Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRVLCYTS 16

93 LLGIWCGSKLICITTA 108

RESULT 13

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S70424; S21992

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70424

A:Status: preliminary

A:Accession: S70424

A:Cross-references: EMBL:X61358; NID:g60177; PIDN:CAA43628.1; PID:g60178

A:Experimental source: patient 22

C:Superfamily: type E retrovirus env polyprotein

Query Match 65.9%; Score 60; DB 2; Length 357;

Best Local Similarity 56.2%; Pred. No. 0.096;

Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRVLCYTS 16

93 LLGIWCGSKLICITTA 108

RESULT 14

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C:Accession: S21998; S70425

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by

A:Reference number: S21990

A:Accession: S21998

A:Status: preliminary

A:Accession: S21998

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70425

A:Status: preliminary

A:Accession: S70425

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

C:Superfamily: type E retrovirus env polyprotein

Query Match 65.9%; Score 60; DB 2; Length 358;

Best Local Similarity 56.2%; Pred. No. 0.096;

Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRVLCYTS 16

94 LLGIWCGSKLICITTA 109

RESULT 15

env polyprotein P - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polyprotein

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999

C:Accession: C41621

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: C41621

A:Status: preliminary

A:Cross-references: GB:M77230; NID:g328631; PIDN:AB03792.1; PID:g555015

A:Note: this virus was isolated from the mother's sexual partner

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:424-443/Domain: transmembrane #status predicted <TMN>

F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 65.9%; Score 60; DB 2; Length 443;

Best Local Similarity 56.2%; Pred. No. 0.11;

Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRVLCYTS 16

332 LLGIWCGSKLICITTA 347

Search completed: May 29, 2003, 10:40:25

Job time : 8.87302 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:31:50 ; Search time 3.93651 Seconds

(without alignments)
168.581 Million cell updates/sec

Title: US-09-147-362a-9

Perfect score: 91

Sequence: 1 ULSWGCKGRVCTYS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	69.2	854	1 ENV_SIVCZ	P17281 chimpanzee
2	60	65.9	843	1 ENV_HV1Y2	P35961 human immun
3	60	65.9	847	1 ENV_HV1S1	P19550 human immun
4	60	65.9	847	1 ENV_HV1W2	P05880 human immun
5	60	65.9	851	1 ENV_HV1B8	P04580 human immun
6	60	65.9	852	1 ENV_HV1BN	P12488 human immun
7	60	65.9	852	1 ENV_HV1S3	P19549 human immun
8	60	65.9	853	1 ENV_HV1M3	P19551 human immun
9	60	65.9	853	1 ENV_HV1M2	P12487 human immun
10	60	65.9	855	1 ENV_HV1A2	P03378 human immun
11	60	65.9	855	1 ENV_HV1OY	P03088 human immun
12	60	65.9	855	1 ENV_HV1Z6	P04579 human immun
13	60	65.9	856	1 ENV_HV1B1	P03375 human immun
14	60	65.9	856	1 ENV_HV1H2	P04578 human immun
15	60	65.9	856	1 ENV_HV1LW	P07026 human immun
16	60	65.9	856	1 ENV_HV1MN	P05877 human immun
17	60	65.9	856	1 ENV_HV1PV	P03376 human immun
18	60	65.9	856	1 ENV_HV1SC	P05879 human immun
19	60	65.9	856	1 ENV_HV1M1	P31872 human immun
20	60	65.9	857	1 ENV_HV2KR	Q74126 human immun
21	60	65.9	861	1 ENV_HV1BR	P03377 human immun
22	60	65.9	865	1 ENV_HV1RH	P12489 human immun
23	60	65.9	867	1 ENV_HV1J3	P12489 human immun
24	60	65.9	868	1 ENV_HV1C4	P05879 human immun
25	58	63.7	848	1 ENV_HV1C4	P20871 human immun
26	58	63.7	856	1 ENV_HV1H3	P04624 human immun
27	58	63.7	856	1 ENV_HV2NZ	P05883 human immun
28	57	62.6	821	1 ENV_SIVGB	P22180 simian immu
29	57	62.6	856	1 ENV_HV1ZH	P05881 human immun
30	56	61.5	846	1 ENV_HV1ND	P18789 human immun
31	55	60.4	712	1 ENV_HV2S2	P32536 human immun
32	55	60.4	846	1 ENV_HV2SB	P12449 human immun
33	55	60.4	851	1 ENV_HV2D1	P17755 human immun

34	55	60.4	851	1 ENV_HV2G1	P18040 human immun
35	55	60.4	858	1 ENV_HV2RO	P04577 human immun
36	55	60.4	859	1 ENV_HV2CA	P24105 human immun
37	55	60.4	859	1 ENV_HV2D2	P15831 human immun
38	55	60.4	859	1 ENV_HV2ST	P20872 human immun
39	55	60.4	860	1 ENV_HV2BE	P18094 human immun
40	55	60.4	885	1 ENV_SIVS4	P12492 simian immu
41	55	60.4	889	1 ENV_SIVS6	P19503 simian immu
42	54	59.3	861	1 ENV_HV1KB	P31819 human immun
43	53	58.2	853	1 ENV_HV1EL	P04581 human immun
44	53	58.2	854	1 ENV_SIVAI	O02837 simian immu
45	53	58.2	859	1 ENV_HV1MA	P04583 human immun

ALIGNMENTS

RESULT 1	ENV_SIVCZ	STANDARD:	PRT:	854 AA.
ID	ENV_SIVCZ	P17281,		
AC	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope polypeptide Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].			
GN	ENV.			
OS	Chimpanzee immunodeficiency virus (SIV(GP2)) (CIV).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
OX	NCBI_Taxid=11723;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90259077; PubMed=218136;			
RA	Huet T., Cheyrier R., Meyers A., Roelance G., Wain-Hobson S.;			
RT	"Genetic organization of a chimpanzee lentivirus related to HIV-1.";			
RL	Nature 345:356-359(1990).			
CC	-I- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPROTEIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; X52154; CA36407.1; -			
DR	PIR; S09990; VCLSI.			
DR	HIV; X52154; ENVSCP2.			
DR	InterPro; IPR000328; ENV GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.			
FT	CHAIN	1	30	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	31	500	TRANSMEMBRANE GLYCOPROTEIN.
FT	CHAIN	501	854	POTENTIAL.
FT	TRANSMEM	501	517	POTENTIAL.
FT	TRANSMEM	675	693	POTENTIAL.
FT	TRANSMEM	805	821	POTENTIAL.
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	143	143	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	260	260	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	267	267	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	299	299	N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match
Best Local Similarity 56.2%; Score 63; DB 1; Length 854;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGCKGRVLYCTS 16
582 ILGLWGCKGKAVCYTT 597

RESULT 2
ENV_HV1Y2 STANDARD; PRT; 843 AA.
AC P35961;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H., Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence for limited defectiveness and complementation.";
RL J. Virol. 66:6587-6600 (1992).

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DR EMBL; M93258; -; NOT_ANNOTATED_CDS.
DR PIR; H44001; H44001.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Glycoprotein; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 489
FT CHAIN 430 843
FT TRANSMEM TRANSMEMBRANE GLYCOPROTEIN.
FT TRANSMEM 738 755
FT DISULFID 53 73
FT DISULFID 118 201
FT DISULFID 125 192
FT DISULFID 130 155
FT DISULFID 214 243
DR BY SIMILARITY.

FT DISULFID 224 235 BY SIMILARITY.
FT DISULFID 252 326 BY SIMILARITY.
FT DISULFID 373 432 BY SIMILARITY.
FT DISULFID 380 405 BY SIMILARITY.
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 138 138
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 193 193
FT CARBOHYD 230 230
FT CARBOHYD 237 237
FT CARBOHYD 258 258
FT CARBOHYD 272 272
FT CARBOHYD 285 285
FT CARBOHYD 291 291
FT CARBOHYD 297 297
FT CARBOHYD 327 327
FT CARBOHYD 351 351
FT CARBOHYD 381 381
FT CARBOHYD 389 389
FT CARBOHYD 395 395
FT CARBOHYD 400 400
FT CARBOHYD 435 435
FT CARBOHYD 450 450
FT CARBOHYD 598 598
FT CARBOHYD 603 603
FT CARBOHYD 612 612
FT CARBOHYD 624 624
FT CARBOHYD 803 803
SQ SEQUENCE 843 AA; 95648 MW; C69DF971C918B71 CRC64;

Query Match
Best Local Similarity 56.2%; Score 60; DB 1; Length 843;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVLYCTS 16
579 ILGLWGCKGKICITTT 594

RESULT 3
ENV_HV1S1 STANDARD; PRT; 847 AA.
ID ENV_HV1S1
AC P19550;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398 (1990).

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DR EMBL; M65024; AAA45072.1; -.

[illegible]

FT	DISULFID	376	439	BY SIMILARITY.
FT	DISULFID	383	412	BY SIMILARITY.
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	197	197	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	234	234	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	241	241	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	262	262	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	276	276	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	289	289	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	301	301	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	354	354	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	360	360	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	384	384	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	390	390	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	396	396	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	442	442	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	456	456	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	607	607	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	612	612	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	621	621	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	633	633	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	670	670	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	812	812	N-LINKED (GLCNAC. . .) (POTENTIAL)
SO	SEQUENCE	852 AA;	97203 MW;	2BB866345DEC915F CRC64;

Query Match
 Best Local Similarity 56.2%; Score 60; DB 1; Length 852;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTS 16
 588 LLSWGCKGRIVCYTS 603

RESULT 7
 ENV_HV153 STANDARD; PRT; 852 AA.
 AC P19549;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV
 OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCB1_TaxID=11690;
 RN [1]
 RP MEDLINE=90317906; PubMed=2370688;
 RX York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
 RA "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";
 RL J. Virol. 64:4016-4020(1990).
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 CC EMBL; M38427; AAA45067.1; -

DR	HIV; M38427; ENVSF33.	31	31	BY SIMILARITY.
DR	InterPro; IPR000328; ENV_GP41.	506	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
DR	InterPro; IPR000777; GP120.	852	852	TRANSMEMBRANE GLYCOPROTEIN.
DR	Pfam; PF00516; GP120; 1.	73	73	BY SIMILARITY.
DR	Pfam; PF00517; GP41; 1.	206	206	BY SIMILARITY.
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.	125	125	BY SIMILARITY.
FT	CHAIN	118	118	BY SIMILARITY.
FT	CHAIN	125	125	BY SIMILARITY.
FT	DISULFID	130	130	BY SIMILARITY.
FT	DISULFID	219	219	BY SIMILARITY.
FT	DISULFID	229	229	BY SIMILARITY.
FT	DISULFID	297	297	BY SIMILARITY.
FT	DISULFID	377	377	BY SIMILARITY.
FT	DISULFID	384	384	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	159	159	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	189	189	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	277	277	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	339	339	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	385	385	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	391	391	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	401	401	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	405	405	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	442	442	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	457	457	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	607	607	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	612	612	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	621	621	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	633	633	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	812	812	N-LINKED (GLCNAC. . .) (POTENTIAL)
SO	SEQUENCE	852 AA;	96663 MW;	EE7B8F8D23C910D CRC64;

Query Match
 Best Local Similarity 56.2%; Score 60; DB 1; Length 852;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRIVCYTS 16
 588 LLSWGCKGRIVCYTS 603

RESULT 8
 ENV_HV153 STANDARD; PRT; 853 AA.
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCB1_TaxID=11704;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE:90317877; PubMed:1695254;
 RA Stevenson M., Haggerty S., Lamonic C., Mann A.M., Meier C.,
 RT "Cloning and characterization of human immunodeficiency virus type 1
 RT variants diminished in the ability to induce syncytium-independent
 RT cytolysis";
 RL J. Virol. 64:3792-3803 (1990).
 CC -----
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 CC -----
 CC EMBL: M3943; AAA44850.1; -
 DR HIV; M3943; ENVSWEA.
 DR Interpro: IPR000328; Env GP41.
 DR Interpro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 509
 FT CHAIN 510 853
 FT DISULFID 54 74
 FT DISULFID 119 203
 FT DISULFID 126 194
 FT DISULFID 131 157
 FT DISULFID 216 245
 FT DISULFID 226 237
 FT DISULFID 294 329
 FT DISULFID 376 443
 FT DISULFID 383 416
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 195 195
 FT CARBOHYD 232 232
 FT CARBOHYD 239 239
 FT CARBOHYD 260 260
 FT CARBOHYD 274 274
 FT CARBOHYD 287 287
 FT CARBOHYD 293 293
 FT CARBOHYD 299 299
 FT CARBOHYD 330 330
 FT CARBOHYD 354 354
 FT CARBOHYD 384 384
 FT CARBOHYD 390 390
 FT CARBOHYD 395 395
 FT CARBOHYD 404 404
 FT CARBOHYD 446 446
 FT CARBOHYD 461 461
 FT CARBOHYD 609 609
 FT CARBOHYD 614 614
 FT CARBOHYD 623 623
 FT CARBOHYD 635 635
 FT CARBOHYD 672 672
 FT CARBOHYD 748 748
 FT CARBOHYD 814 814
 FT SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;
 Query Match 65.9%; Score 60; DB 1; Length 853;
 Beat Local Similarity 56.2%; Pred. No. 0.04;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 590 LIGTWCSCGKLCITTA 605
 RESULT 9
 ENV_HV122
 ID ENV_HV122 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z2/CDC-Z34 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Theodore T., Buckler-White A.;
 RL Submitted (NOV-1988) to the HIV data bank.
 CC -----
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 CC -----
 CC EMBL: M2639; AAA45370.1; -
 DR HIV; M2639; ENV52226.
 DR Interpro: IPR000328; Env GP41.
 DR Interpro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 508
 FT CHAIN 509 853
 FT DISULFID 53 73
 FT DISULFID 118 206
 FT DISULFID 125 197
 FT DISULFID 130 154
 FT DISULFID 219 248
 FT DISULFID 229 240
 FT DISULFID 297 330
 FT DISULFID 376 442
 FT DISULFID 383 415
 FT CARBOHYD 87 87
 FT CARBOHYD 137 137
 FT CARBOHYD 144 144
 FT CARBOHYD 153 153
 FT CARBOHYD 157 157
 FT CARBOHYD 185 185
 FT CARBOHYD 188 188
 FT CARBOHYD 198 198
 FT CARBOHYD 235 235
 FT CARBOHYD 242 242
 FT CARBOHYD 263 263
 FT CARBOHYD 277 277
 FT CARBOHYD 290 290
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 FT CARBOHYD 331 331
 FT CARBOHYD 338 338
 FT CARBOHYD 353 353
 FT CARBOHYD 384 384
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 FT CARBOHYD 402 402
 FT CARBOHYD 441 441
 FT CARBOHYD 445 445
 FT CARBOHYD 458 458
 FT SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;
 Query Match 65.9%; Score 60; DB 1; Length 853;
 Beat Local Similarity 56.2%; Pred. No. 0.04;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

FT	CARBOHYD	154	154	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	184	184	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	190	190	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	200	200	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	223	223	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	244	244	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	265	265	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	279	279	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	304	304	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	334	334	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	341	341	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	358	358	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	364	364	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	388	388	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	394	394	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	408	408	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	445	445	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	461	461	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	610	610	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	615	615	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	636	636	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	815	815	N-LINKED (GLCNAC. .)	(POTENTIAL)
SO	SEQUENCE	855 AA;	97438 MW;	A3BC20573AAC41A2 CRC64;	
Query Match	Best Local Similarity	65.9%;	Score 60;	DB 1;	Length 855;
Matches	9;	Conservative	3;	Mismatches	4;
				Indels	0;
				Gaps	0;
Oy	1				
Db	591	LLSGMGCKRLVCYTS	16		
		LLGIWGCGSKLICITTA	606		
RESULT 11					
ENV_HV10Y					
ID	ENV_HV10Y	STANDARD;	PRT;	855 AA.	
AC	P20888;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].				
DE	ENV.				
OS	Human immunodeficiency virus type 1 (OY1 isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11699;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=90148544; PubMed=2559749;				
RA	Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;				
RT	"A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";				
RL	AIDS 3:707-715(1989).				
CC	-1- MISCELLANEOUS: THE OY1 ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb.ch/announce/isb.ch).				
CC	or send an email to license@isb-sib.ch).				
DR	EMBL; M26727; AAA83397.1; -				
DR	HIV; M26727; ENV5OY1.				
DR	InterPro; IPR000328; Env_GP41.				

DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 509
 FT CHAIN 510 855
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 223 252
 FT DISULFID 301 335
 FT DISULFID 381 442
 FT DISULFID 381 442
 FT CARBOHYD 87 87
 FT CARBOHYD 134 134
 FT CARBOHYD 142 142
 FT CARBOHYD 145 145
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
 FT CARBOHYD 192 192
 FT CARBOHYD 202 202
 FT CARBOHYD 239 239
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 284 284
 FT CARBOHYD 300 300
 FT CARBOHYD 306 306
 FT CARBOHYD 336 336
 FT CARBOHYD 359 359
 FT CARBOHYD 389 389
 FT CARBOHYD 395 395
 FT CARBOHYD 399 399
 FT CARBOHYD 405 405
 FT CARBOHYD 458 458
 FT CARBOHYD 610 610
 FT CARBOHYD 615 615
 FT CARBOHYD 624 624
 FT CARBOHYD 636 636
 FT CARBOHYD 815 815
 SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607AD6D2DA CRC64;
 Query Match 65.9%; Score 60; DB 1; Length 855;
 at Local Similarity 56.2%; Pred. No. 0.04;
 tches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LLSWGCKGRVLYCTYS 16
 DB 591 LLSWGCKGRVLYCTYS 606
 ID ENV_HV126 STANDARD; PRT; 855 AA.
 AC P04580;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor (Contaminant: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN Env.
 OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
 OC Viruses; Retrovirus; Retroviridae; Lentivirus.
 OC NCBI_TaxId=11708;
 RX MEDLINE=87248097; PubMed=3036660;
 RA Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
 Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,

RA Sanchez-Pescador R.;
 RT "Molecular characterization of human immunodeficiency virus from
 RT Zaire: nucleotide sequence analysis identifies conserved and variable
 RT domains in the envelope gene."
 RL Gene 52:71-82(1987).
 CC -----
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 CC -----
 DR EMBL; K03458; AAA5380.1; -
 DR PIR; D26192; VCLJZR.
 DR HIV; K03458; ENV526.
 DR InterPro; IPR000777; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 510
 FT CHAIN 511 855
 FT DISULFID 53 73
 FT DISULFID 118 207
 FT DISULFID 125 198
 FT DISULFID 130 155
 FT DISULFID 220 249
 FT DISULFID 230 241
 FT DISULFID 298 332
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 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 140 140
 FT CARBOHYD 145 145
 FT CARBOHYD 154 154
 FT CARBOHYD 158 158
 FT CARBOHYD 186 186
 FT CARBOHYD 189 189
 FT CARBOHYD 199 199
 FT CARBOHYD 236 236
 FT CARBOHYD 243 243
 FT CARBOHYD 264 264
 FT CARBOHYD 278 278
 FT CARBOHYD 291 291
 FT CARBOHYD 297 297
 FT CARBOHYD 333 333
 FT CARBOHYD 340 340
 FT CARBOHYD 355 355
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 398 398
 FT CARBOHYD 404 404
 FT CARBOHYD 443 443
 FT CARBOHYD 447 447
 FT CARBOHYD 460 460
 FT CARBOHYD 461 461
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 FT CARBOHYD 636 636
 FT CARBOHYD 673 673
 SQ SEQUENCE 855 AA; 96971 MW; 3B4D3D6E239C3457 CRC64;
 Query Match 65.9%; Score 60; DB 1; Length 855;
 Best Local Similarity 56.2%; Pred. No. 0.04;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 L155WCKGRVLYCYS 16
DB 591 L155WCKGRVLYCYS 606

RESULT 13
ENV_HV1B1 STANDARD; PRT; 856 AA.

AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11678;

SEQUENCE FROM N.A.
MEDLINE=85111123; PubMed=2578615;
Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Joseph S.F., Doran B.R., Rafalski J.A., Whitehorn E.A., Baumanister K., Ivanoff L., Pettey S.R., Pearson M.L., Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;
"Complete nucleotide sequence of the AIDS virus, HTLV-III.";
Nature 313:277-284 (1985).

RA DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
MEDLINE=90285159; PubMed=2355006;
Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N., Gregory T.J.;
"Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in Chinese hamster ovary cells.";
J. Biol. Chem. 265:10373-10382 (1990).

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CC EMBL, M15654; AAA44205.1; -
PIR; A03973; VCLDH3.
HIV; M15654; ENVSH102.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000772; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Glycoprotein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 34 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160

EXTERIOR MEMBRANE GLYCOPROTEIN.
TRANSMEMBRANE GLYCOPROTEIN.

FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A1931BB27 CIRC64;

Query Match Score 60; DB 1; Length 856;
Best Local Similarity 56.2%; Pred. No. 0.04;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 L155WCKGRVLYCYS 16
DB 592 L155WCKGRVLYCYS 607

RESULT 14
ENV_HV1B2 STANDARD; PRT; 856 AA.

AC 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11706;

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CC EMBL, K03455; AAB50262.1; -

Query Match 65.9%; Score 60; DB 1; Length 856;
Best Local Similarity 56.2%; Pred. No. 0.04;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ILSSWGCKGRIVCYTS 16
||| ||| :||| :
Db 592 ILGIWGCSGKLICTTA 607

Search completed: May 29, 2003, 10:36:59
Job time : 3.93651 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:32:35 ; Search time 16.5079 seconds
(without alignments)
199.707 Million cell updates/sec

Title: US-09-147-362A-9
Perfect score: 91
Sequence: 1 LLSWGCKRLVCYTS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPTREMBL_21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	96.7	216	15 Q91EC5	Q91EC5 human immun
2	88	96.7	219	15 Q91EB6	Q91EB6 human immun
3	88	96.7	890	15 Q807G2	Q807G2 human immun
4	87	95.6	218	15 Q91E95	Q91E95 human immun
5	87	95.6	538	15 Q91ED5	Q91ED5 human immun
6	86	94.5	219	15 Q91EC8	Q91EC8 human immun
7	85	93.4	130	15 Q91HU9	Q91HU9 human immun
8	85	93.4	216	15 Q91EC7	Q91EC7 human immun
9	85	93.4	535	15 Q91EF2	Q91EF2 human immun
10	85	93.4	872	15 Q807H0	Q807H0 human immun
11	85	93.4	882	15 Q807F9	Q807F9 human immun
12	85	93.4	887	15 Q807H6	Q807H6 human immun
13	85	93.4	887	15 Q807G9	Q807G9 human immun
14	84	92.3	135	15 Q9DOL9	Q9DOL9 human immun
15	84	92.3	209	15 Q91EB6	Q91EB6 human immun
16	84	92.3	242	15 Q91E31	Q91E31 human immun

17	82	90.1	116	15 Q40459	Q40459 human immun
18	82	90.1	118	15 Q40451	Q40451 human immun
19	82	90.1	140	15 Q91HU2	Q91HU2 human immun
20	82	90.1	131	15 Q9WR05	Q9WR05 human immun
21	82	90.1	131	15 Q91HU0	Q91HU0 human immun
22	82	90.1	137	15 Q91HV5	Q91HV5 human immun
23	82	90.1	146	15 Q9WRV2	Q9WRV2 human immun
24	82	90.1	213	15 Q91EC3	Q91EC3 human immun
25	82	90.1	214	15 Q91E96	Q91E96 human immun
26	82	90.1	214	15 Q9D1K3	Q9D1K3 human immun
27	82	90.1	216	15 Q91EA5	Q91EA5 human immun
28	82	90.1	230	15 Q91EA9	Q91EA9 human immun
29	82	90.1	234	15 Q91EA6	Q91EA6 human immun
30	82	90.1	342	15 Q11942	Q11942 human immun
31	82	90.1	529	15 Q91EE2	Q91EE2 human immun
32	82	90.1	532	15 Q91EE9	Q91EE9 human immun
33	82	90.1	544	15 Q91ED9	Q91ED9 human immun
34	82	90.1	548	15 Q91ED6	Q91ED6 human immun
35	82	90.1	551	15 Q91EB1	Q91EB1 human immun
36	82	90.1	863	15 Q77377	Q77377 human immun
37	82	90.1	867	15 Q807G8	Q807G8 human immun
38	82	90.1	871	15 Q57073	Q57073 human immun
39	82	90.1	871	15 Q57074	Q57074 human immun
40	82	90.1	871	15 Q807I2	Q807I2 human immun
41	82	90.1	872	15 Q57072	Q57072 human immun
42	82	90.1	872	15 Q900Y5	Q900Y5 human immun
43	82	90.1	900	15 Q9QNZ8	Q9QNZ8 human immun
44	81	89.0	111	15 Q40455	Q40455 human immun
45	81	89.0	114	15 Q40448	Q40448 human immun

ALIGNMENTS

RESULT 1

Q91EC5 ID Q91EC5 PRELIMINARY; PRT; 216 AA.
AC Q91EC5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=BCF07;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
DR EMBL, AJ236394; CAB96243.1.
DR InterPro; IPR000328; ENV_GP41.
DR Pfam; PF00517; GP41; 1.
FT Transmembrane.
KW NON_TER
FT NON_TER
SQ SEQUENCE 216 AA; 25027 MW; 413AB9BBF1B4FC9A CRC64;

Query Match 96.7%; Score 88; DB 15; Length 216;
Best Local Similarity 93.8%; Pred. No. 3.2e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0;

QY 1 LLSWGCKRLVCYTS 16
||:|||||
Db 47 LLSWGCKRLVCYTS 62

RESULT 2
Q91EB6 PRELIMINARY; PRT; 219 AA.

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AC Q9IEB6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN GP41 (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCF14;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ236404; CAB96252.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER
FT NON_TER
SQ SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

Query Match
Best Local Similarity 96.7%; Score 88; DB 15; Length 219;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
DB 57 LLSWGCKGRIVCYTS 72

RESULT 3
O807G2 PRELIMINARY; PRT; 890 AA.
AC O807G2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97US08692A;
RA Yamauchi J., Vallari A.S., Swanson P., Bodelle P., Kapur L.,
RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
RT Phylogenetic Clusters.";
RL AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL; AF383259; AAL98881.1; -
DR SEQUENCE 890 AA; 100610 MW; BBE816BC5C45EE23 CRC64;

Query Match
Best Local Similarity 96.7%; Score 88; DB 15; Length 890;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
DB 620 LLSWGCKGRIVCYTS 635

RESULT 4
O9IE95 PRELIMINARY; PRT; 218 AA.
AC O9IE95;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

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DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF51;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ236425; CAB96273.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER
FT NON_TER
SQ SEQUENCE 218 AA; 25243 MW; E7F0E1E20EF79FA8 CRC64;

Query Match
Best Local Similarity 95.6%; Score 87; DB 15; Length 218;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
DB 54 LLSWGCKGRIVCYTS 69

RESULT 5
O9IED5 PRELIMINARY; PRT; 538 AA.
AC O9IED5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF51;
RA Roques P., Robertson D., Diamond F., Souquiere S., Mauciere P.,
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region.";
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ133072; CAB96233.1; -
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER
FT NON_TER
SQ SEQUENCE 538 AA; 60777 MW; B3C9B66A23FEFD CRC64;

Query Match
Best Local Similarity 95.6%; Score 87; DB 15; Length 538;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCYTS 16
DB 374 LLSWGCKGRIVCYTS 389

RESULT 6
O9IEC8 PRELIMINARY; PRT; 219 AA.
AC O9IEC8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

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DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF02;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
  Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AJ236391; CAB96240.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 219 219
SQ SEQUENCE 219 AA; 25363 MW; 85C2DC5B5F528907 CRC64;
Query Match
Best Local Similarity 94.5%; Score 86; DB 15; Length 219;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCYTS 16
DB 56 LLSWGCKGRLVCYTS 71

RESULT 7
O9IHU9
ID O9IHU9 PRELIMINARY; PRT; 130 AA.
AC O9IEF2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE Env1ope glycoprotein (Fragment).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CM798;
RX MEDLINE=20386754; PubMed=10933623;
RA Yang C., Gao F., Rojunga P.N., Zekeng L., van der Groen G.,
  Pieniazek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
  type 1 group O.";
  Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AF29235; AAF71912.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 15593 MW; 5385789A336344EA CRC64;
Query Match
Best Local Similarity 93.4%; Score 85; DB 15; Length 130;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCYTS 16
DB 40 LLSWGCKGRLVCYTS 55

RESULT 8
O9IEC7
ID O9IEC7 PRELIMINARY; PRT; 216 AA.
AC O9IEC7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
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DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF03;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
  Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AJ236392; CAB96241.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 216 216
SQ SEQUENCE 216 AA; 25015 MW; 780C5F39CA6997C2 CRC64;
Query Match
Best Local Similarity 93.4%; Score 85; DB 15; Length 216;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCYTS 16
DB 55 LLSWGCKGRLVCYTS 70

RESULT 9
O9IEF2
ID O9IEF2 PRELIMINARY; PRT; 535 AA.
AC O9IEF2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE Env polypeptide (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF03;
RA Roques P., Robertson D., Diamond F., Souquiere S., Mauciere P.,
  Depierre C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region.";
  Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AJ133055; CAB96216.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
FT NON_TER 535 535
SQ SEQUENCE 535 AA; 59682 MW; 7234BB8378DD12C5 CRC64;
Query Match
Best Local Similarity 93.8%; Score 85; DB 15; Length 535;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCYTS 16
DB 374 LLSWGCKGRLVCYTS 389

RESULT 10
O807H0
ID O807H0 PRELIMINARY; PRT; 872 AA.
AC O807H0;
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DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CMA124;
RX MEDLINE=21849375; PubMed=11860674;
RA Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kapue L.,
RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
RT Phylogenetic Clusters."
RL AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL; AF383251; AAL98873.1;
SQ SEQUENCE 872 AA; 98344 MW; 91D37F6053827E3 CRC64;

Query Match 93.4%; Score 85; DB 15; Length 872;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCTYS 16
DB 602 LLSWGCKGRLVCTYS 617

RESULT 11
O807F9 PRELIMINARY; PRT; 882 AA.
AC O807F9;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CMA100;
RX MEDLINE=21849375; PubMed=11860674;
RA Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kapue L.,
RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
RT Phylogenetic Clusters."
RL AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL; AF383252; AAL98884.1;
SQ SEQUENCE 882 AA; 99439 MW; 627BCA5D0C09C6D4 CRC64;

Query Match 93.4%; Score 85; DB 15; Length 882;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCTYS 16
DB 613 LLSWGCKGRLVCTYS 628

RESULT 12
O807H6 PRELIMINARY; PRT; 887 AA.
AC O807H6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
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OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CMA124;
RX MEDLINE=21849375; PubMed=11860674;
RA Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kapue L.,
RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
RT Phylogenetic Clusters."
RL AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL; AF383245; AAL98867.1;
SQ SEQUENCE 887 AA; 99366 MW; E210F1E3F7B2474D CRC64;

Query Match 93.4%; Score 85; DB 15; Length 887;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCTYS 16
DB 618 LLSWGCKGRLVCTYS 633

RESULT 13
O807G9 PRELIMINARY; PRT; 887 AA.
AC O807G9;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CMA114;
RX MEDLINE=21849375; PubMed=11860674;
RA Yamaguchi J., Vallari A.S., Swanson P., Bodelle P., Kapue L.,
RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
RT Phylogenetic Clusters."
RL AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL; AF383252; AAL98874.1;
SQ SEQUENCE 887 AA; 99559 MW; 88954F4ED76A31A4 CRC64;

Query Match 93.4%; Score 85; DB 15; Length 887;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCTYS 16
DB 618 LLSWGCKGRLVCTYS 633

RESULT 14
O807G9 PRELIMINARY; PRT; 135 AA.
AC O807G9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP-M1321;
RX MEDLINE=20584646; PubMed=11153079;
RA Ortiz M., Munoz L., Bernal A., Rodriguez A., Zorranguino A.,
RA Vadillo J., Salas A., Moreno A., Garcia-Salz A.,
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